



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number 140730

To: Sarvamangala Devi  
Location: REM 3C18  
Art Unit: 1645  
Monday, December 20, 2004

Case Serial Number: 10/696544

From: Beverly Shears  
Location: Remsen Bldg.  
RM 1A54  
Phone: 571-272-2528

beverly.shears@uspto.gov

### Search Notes

Shears, Beverly

140730

From: Devi, Sarvamangala  
Sent: Thursday, December 16, 2004 9:46 AM  
To: Shears, Beverly  
Subject: 10/696,544

Good morning Beverly:

Please perform a sequence search for SEQ ID NO: 2 ~~both~~ in commercial and interference databases in application 10/696,544. Please include an inventors' name search for Anthony W. Confer; Sahlu Ayalew; George L. Murphy; and Karamjeet Pandher.

Thanx.

S. DEVI, Ph.D.  
Primary Examiner  
AU 1645  
Rems - 3C18



Date completed:

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

### Search Site

\_\_\_\_ STIC

\_\_\_\_ CM-1

\_\_\_\_ Pre-S

### Type of Search

\_\_\_\_ N.A. Sequence

\_\_\_\_ A.A. Sequence

\_\_\_\_ Structure

\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_ IC

\_\_\_\_ STN

\_\_\_\_ Dialog

\_\_\_\_ APS

\_\_\_\_ Geninfo

\_\_\_\_ SDC

\_\_\_\_ DARC/Questel

\_\_\_\_ ☒ Other CGN

**This Page Blank (uspto)**

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 17, 2004, 15:52:32 ; Search time 221.711 Seconds  
(without alignments)  
874.569 Million cell updates/sec

Title: US-10-696-544-2

Perfect score: 1734

Sequence: 1 CGSGSGSGSSSTPNHPKPV.....YLIGEAQSDNQAIMVSEKK 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1734	100.0	356	2 Q9ZHK7	Q9ZHK7 pasteurella
2	270	15.6	348	2 Q9CKT8	Q9CKT8 pasteurella
3	221.5	12.8	335	2 Q9CKT9	Q9CKT9 pasteurella
4	177	10.2	1158	2 Q6JSM4	Q6JSM4 streptococc
5	177	10.2	1158	2 AAT10376	AAT10376 streptoco
6	174	10.0	331	2 Q9CKU2	Q9CKU2 pasteurella
7	173	10.0	1083	2 Q75WB4	Q75WB4 streptococc
8	173	10.0	1083	2 BAC98831	BAC98831 streptoco
9	173	10.0	1134	2 Q99051	Q99051 streptococc
10	173	10.0	1164	1 BAG_STRAG	P27951 streptococc
11	172	9.9	1443	2 Q8T1B6	Q8T1B6 dictyosteli
12	171.5	9.9	201	2 O15691	O15691 plasmodium
13	162	9.3	405	2 Q8BMN8	Q8BMN8 mus musculu
14	162	9.3	761	2 Q8ZP12	Q8ZP12 mus musculu
15	162	9.3	761	2 BAC98253	BAC98253 mus muscu
16	162	9.3	883	2 Q8HLB7	Q8HLB7 mus musculu
17	160.5	9.3	365	2 Q9RCG1	Q9RCG1 actinobacil
18	159.5	9.2	365	1 OMLA_ACTPL	Q02937 actinobacil
19	159.5	9.2	365	2 Q9R3L8	Q9R3L8 actinobacil
20	159.5	9.2	896	2 P91448	P91448 caenorhabdi
21	155	8.9	375	2 Q9RCG2	Q9RCG2 actinobacil
22	149	8.6	194	2 O15687	O15687 plasmodium
23	147.5	8.5	364	2 Q9R3S1	Q9R3S1 actinobacil
24	147	8.5	368	2 Q9RCG3	Q9RCG3 actinobacil
25	147	8.5	368	2 Q9RIH8	Q9RIH8 actinobacil
26	147	8.5	837	2 Q9VYU7	Q9VYU7 drosophila
27	143.5	8.3	213	2 Q9VU17	Q9VU17 streptococc
28	143.5	8.3	365	2 Q9R3V2	Q9R3V2 actinobacil
29	143	8.2	1364	2 Q8T245	Q8T245 dictyosteli
30	142.5	8.2	677	1 BACS_BOHMO	Q9B1J6 bombyx mori
31	141	8.1	3164	1 T8GU_HHV11	P10220 human herpe

32 140.5 8.1 730 2 Q9X6U0 Q9X6U0 streptococc  
33 140 8.1 219 2 Q7X576 Q7X576 streptococc  
34 139 8.0 249 2 Q7X579 Q7X579 streptococc  
35 139 8.0 255 2 Q7X578 Q7X578 streptococc  
36 139 8.0 1309 2 Q6CCL1 Q6CCL1 yarrowia li  
37 138.5 8.0 201 2 Q7X584 Q7X584 streptococc  
38 138.5 8.0 366 2 Q44163 Q44163 actinobacil  
39 138.5 8.0 367 2 Q44164 Q44164 actinobacil  
40 138.5 8.0 367 2 Q9ZAP9 Q9ZAP9 actinobacil  
41 137.5 7.9 201 2 Q8VSU5 Q8VSU5 streptococc  
42 137 7.9 249 2 Q8VST7 Q8VST7 streptococc  
43 136 7.8 219 2 Q7X580 Q7X580 streptococc  
44 136 7.8 379 2 Q95WF2 Q95WF2 drosophila  
45 135.5 7.8 165 2 Q8GAP7 Q8GAP7 streptococc

## ALIGNMENTS

### RESULT 1

Q9ZHK7 PRELIMINARY; PRT; 356 AA.  
ID Q9ZHK7  
AC Q9ZHK7;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-MAY-2004 (Tremblrel. 26, Last annotation update)  
DE Outer membrane lipoprotein PipE.  
GN Name=plpE;  
OS Pasteurella haemolytica.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Mannheimia.  
OX NCBI\_TaxID=75985;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=89010807N;  
RX MEDLINE=99043883; PubMed=9826333;  
RA Pandher K., Confer A.W., Murphy G.L.;  
RT "Genetic and immunologic analyses of PipE, a lipoprotein important in complement-mediated killing of Pasteurella haemolytica serotype 1.";  
RL Infect. Immun. 66:5613-5619 (1998).  
DR EMBL; AF059036; AAC82640.1;  
DR InterPro; IPR005014; Lipoprotein\_14.  
DR Pfam; PF03346; Lipoprotein\_14; 1.  
KW Lipoprotein.  
SQ SEQUENCE 356 AA; 39129 MW; E66E48DFE87393D7 CRC64;

Query Match 100.0%; Score 1734; DB 2; Length 356;  
Sest Local Similarity 100.0%; Pred. No. 1.7e-97;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGSGSGSGSSSTPNHPKPVLPVPTQNNLQANVPQANASQAQNAQANAPQV 60  
DB 20 CGSGSGSGSSSTPNHPKPVLPVPTQNNLQANVPQANASQAQNAQANAPQV 79  
QY 61 ENAQANAPQANAPQANAPQANAPQANAPQANAPQANAPQANAPQV 120  
DB 80 ENAQANAPQANAPQANAPQANAPQANAPQANAPQANAPQANAPQV 139  
QY 121 KLGTTPKPKVSGKKIIEEKDFVLNLSDNAQSGDFLIRSDDLFYGYHDTNGKNL 180  
DB 140 KLGTTPKPKVSGKKIIEEKDFVLNLSDNAQSGDFLIRSDDLFYGYHDTNGKNL 199  
QY 181 VDADKTSQYFVYDEKRVNDNSDKLTATYRKKEGVPVGSNPHTEFAARIKSLGDEI 240  
DB 200 VDADKTSQYFVYDEKRVNDNSDKLTATYRKKEGVPVGSNPHTEFAARIKSLGDEI 259  
QY 241 KFGNQAGSGIKDKGNAIFITIKGTQKOLEITPTESNRIIAILDQNKSYTPGMEKA 300  
DB 260 KFGNQAGSGIKDKGNAIFITIKGTQKOLEITPTESNRIIAILDQNKSYTPGMEKA 319  
QY 301 IMETKFDISKAGNSDQKYLIGEAQSDNQAIMVSEKK 337  
DB 320 IMETKFDISKAGNSDQKYLIGEAQSDNQAIMVSEKK 356

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RESULT 2
Q9CKT8      PRELIMINARY;      PRT;      348 AA.
AC Q9CKT8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PipP.
GN Name=plpP; OrderedLocusNames=PM1518;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Faustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006188; AAK03602.1; -.
DR EMBL; AE006188; AAK03601.1; -.
DR Complete proteome.
SQ SEQUENCE 348 AA; 37362 MW; DCB2191499653F52 CRC64;

Query Match      15.6%; Score 270; DB 2; Length 348;
Best Local Similarity 25.8%; Pred. No. 1.5e-08;
Matches 97; Conservative 51; Mismatches 128; Indels 100; Gaps 17;

QY 1 CGGSGGSSSTPHPKPVLPKTONNLAQNVPQASQAQNAPOAQNAPQV 60
DB 21 CGGGGGSGNGNAPPFV-----QPIQAPPAHQPPDA--APNI 58
QY 61 ENAPQAQNAPO--VENAQAQAEVTPVP-----QPQS--QKIDGSFDK---IGSVKLN 105
DB 59 P-APKQCAPTGAKAPPAAPPAPAPANDMGMSPPSAQKWEKGAESKVCARKNEN 117
QY 106 KEAOTL-ELSFRTLVK-LGTPPKFKVSGKKIIEKDFLVNLSDINAEQLSGDFLIRR 163
DB 118 KHVTVYKLEHVENADRNSSTPDKYK-----EPEHITLNLGDNNGVYKFTLLGSD 169
QY 164 SDDL-FYGYVHDTNGKLVDAADKFSQYFVYVDEKRVNDNI-----SDKL 207
DB 170 GNEVGYGYRHN-----IDDSRAHKVVELLYAINTDFKSPDQSTQF 210
QY 208 TATYRKKEGFYVGSNPHTKFAARISKLGDEIKFENGQAQGSIKDEKQNA-----EI 261
DB 211 KAVYKKEKGFYAPISNTELSNGLINGVDNLYDNGSISGSIYRSENGSRETWKELI 270
QY 262 FTI-KGDTKQLEITPTESRIIILADQNKSYTPGMEKAIMTKFIDSKAGNSDKYLI 320
DB 271 FKIEKHGSGSTIEP-----VLEHLLGTIKKG-----DKANLNYILADSEKGRADHKYLF 320
QY 321 GEAKSDNQAIMVSEK 336
DB 321 GNAKAETWIGVLAEEK 336

RESULT 3
Q9CKT9      PRELIMINARY;      PRT;      335 AA.
AC Q9CKT9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PipP.
GN Name=plpP; OrderedLocusNames=PM1517;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Faustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006188; AAK03602.1; -.
DR EMBL; AE006188; AAK03601.1; -.
DR Complete proteome.
SQ SEQUENCE 335 AA; 5169813A26F7E7BB CRC64;

Query Match      12.8%; Score 221.5; DB 2; Length 335;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
Matches 79; Conservative 58; Mismatches 160; Indels 49; Gaps 10;

QY 2 GGGSGGSSSTPHPKPVLPKTONNLAQNVPQASQAQNAPOAQNAPQV 61
DB 23 GGGGAGNADRVEEK-----AQPV---QSNSEPSAPIKNPTNTATNDSLHD 67
QY 62 NAQAQNAQVNAQAQAEVTPVPQPOQKIDGSF-----DKTGSVKLANKEAQTLELS 114
DB 68 KLSMSHSDTSKENSQQSSPKALEKQKQPAQENLTWTGYHVSEVGNASNNVVDKNVTV- 126
QY 115 RFTLV---DKLGTTPPKFKVSGKKIIEKDFLVNLSDINAEQLSGDFLIRSDDLFYGY 171
DB 127 -FTFVKYNSQYNDPFDKTKTQS-----KTISLVGKKNENKEDYNYNFTLKDALF-- 175
QY 172 YHDTNGKLVDAADKFSQYFVYVDEKRVNDNISDKLTATYRKKEGFYVGSNPHTKFAAR 231
DB 176 YGSGGQSPADYKVEKNIYIAKPDANNENLNALTATYYQEDGFIYSLVDNVRVSGE 235
QY 232 -ISKLGDEIKFENGQAQGSIKDEKQNAEIFTKGDTKQLEITPTESRIIILADQNK 290
DB 236 YIYQGVNLTITFNGKIYGEIVRYNRRGDDLQSLGEGQNLITPHK-----DNPH 286
QY 291 KSYTGMKAMNETKIDSKAGNSDKYLI GEAKSDNQAIMVSEK 336
DB 287 KLSPTGPDNMAELNFIN--AEKTDKYYVGVGKAEKYIYGLLFAEK 330

RESULT 4
Q6J5M4      PRELIMINARY;      PRT;      1158 AA.
AC Q6J5M4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-antigen.
GN Name=beta;
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=98-D60C;
RA Dmitriev A., Shen A.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
   an amide bond (by similarity).
DR EMBL; AY598359; AAT10376.1; -.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR005877; Gaps_YSIK.
DR InterPro; IPR001899; Gaps_pos_anchor.
DR InterPro; IPR003599; IG.
DR InterPro; IPR011047; Quin_alc_DH_like.
DR InterPro; IPR007756; RICH.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF05062; RICH_1_signal; 1.
DR Pfam; PF04650; YSIK_signal; 1.
DR ProDom; PD153432; Csurface_antigen; 2.
DR SMART; SM00409; IG; 1.

```

Qy	171	YHDTNGKNLVDAADKFSQVFPVVD-----EKRVNDNISDKLTATYRKKEGFVGSN	222
Db	987	---HKTGGGTV-----RVFDI.SLSKGGKETHNGERTVRLALGQTGSDVHVY---	1030
Qy	223	PHTKEFAARISKLDGVE---IKFENGQAQGSIKDEKGNAEIFTIKGTDKOLEITPTESN	279
Db	1031	---HVKE-----NGDLERIPSKVNGQV-----FKTNHFSIFAIKTISKQNVTPPKQT	1077
Qy	280	RIITAILDQNKSYTPGMEKAIMET---KFDISKAGN	313
Db	1078	-----KPSQTQGSQVEIAESQTGKF-QSKAAN	1102
RESULT 6			
ID	Q9CKU2	PRELIMINARY;	PRT; 331 AA.
AC	Q9CKU2;		
DT	01-JUN-2001 (TReMBLrel. 17, Created)		
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)		
DT	01-MAR-2004 (TReMBLrel. 26, Last annotation update)		
DE	Hypothetical protein PM1514.		
GN	OrderedLocusNames=PM1514;		
OS	Pasteurella multocida.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;		
OC	Pasteurellaceae; Pasteurella.		
OX	NCBI_TaxID=747;		
FN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PM70;		
RC	MEDLINE=21145866; PubMed=11248100;		
RT	May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;		
RA	"Complete genomic sequence of Pasteurella multocida Pm70.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).		
DR	EMBL; AB066188; AAK03598.1; --		
KW	Complete proteome; Hypothetical protein.		
SQ	SEQUENCE 331 AA; 37271 MW; 8CC9DAA01EDC4BAA CRC64;		
Query Match 10.0%; Score 174; DB 2; Length 331;			
Best Local Similarity 22.0%; Pred. No. 0.0094;			
Matches 79; Conservative 73; Mismatches 131; Indels 76; Gaps 18;			
Qy	1	CGSGSGSGSSSTPNH-----PKVUL--VPTQNNLQAO-----NVPOAQNASQAQN	44
Db	21	CGSGGGGGGNNNS-NHQAHFVNPVAPLHVAAKPOQHVEQEVIEKKPPVPVTRTASOS--	77
Qy	45	APQAQNAPOAQNAPQVENAPQAQNAQVNAQAEVTPFPQPSQKIDGSDFKIGSVKL	104
Db	78	-----SFYSKAPQSVGHDKRSVHWKGSVSXEHLDFSY-----	112
Qy	105	NKEAQTLELSFTLVDTLGTTPKFDKVSCKK.IIEKD--FLVNLSDINAELSG-DPLI	161
Db	113	SKDA-----VTRHLVTNPNAVSTDPNLI-SKDIKITLTITGVNQNKSGPNFEL	163
Qy	162	RASDD-LFVGYHDTNGKNLVDAAKFSQYFVYVDEKRVNDNISDKLTATYRKKEGFVYG	220
Db	164	NLLDENIYGYTRDSQDMNHE-----NLYVVGFKDAENQDNLQLFTANYQGEFLFSTA	218
Qy	221	SNPTKEPAARISKLGDEVIKPFENGQAQGSIKDEKGNAEIFTIKGTDK--OLEITPTES	278
Db	219	TWNP-----VPVLGXAVLNYKEGAKAEIL-ERDSNYKLFDIYWRPNQAILNPV-A	269
Qy	279	NRITAILDQNKSYTPGMEKAIMETKTFIDSKAGNSDOKYLIGEAKSNQWAIMVSEKK	337
Db	270	ERLPTSDLIIMTRKNSP--DRVITDLHFFIKGO-DNQENKIYVGQGNKYGVLGLEKK	325
RESULT 7			
ID	Q75WB4	PRELIMINARY;	PRT; 1083 AA.
AC	Q75WB4;		
DT	05-JUL-2004 (TReMBLrel. 27, Created)		
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)		



```
RA Heden L., Prithz E., Lindahl G.;
RT "Molecular characterization of an Iga receptor from group B
RT streptococci: Sequence of the gene, identification of a proline-rich
RT region with unique structure and isolation of N-terminal fragments
RT with Iga-binding capacity.";
RL Eur. J. Immunol. 21:1481-1490(1991).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (By similarity).
DR EMBL; X58470; CAA41384.1; -.
DR FIRM; A60234; A60234.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR004829; Csurface_antigen; IEA.
DR InterPro; IPR005877; Gpos_ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR007756; Ig.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007756; RICH.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF05062; RICH; 1.
DR Pfam; PF04650; Ysirk_signal; 1.
DR SMART; SM00409; IG; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Receptor.
SQ SEQUENCE 1134 AA; 127980 MW; FCL0A200B3DB7CE1 CRC64;

Query Match 10.0%; Score 173; DB 2; Length 1134;
Best Local Similarity 23.7%; Pred. No. 0.048;
Matches 76; Conservative 45; Mismatches 110; Indels 90; Gaps 15;

QY 12 TPNHKEVLPVKTQNNLQAQNVFQAQNASQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71
DB 829 TPTDKPIPELPQADPTPQADPTHPVPSKAPAPRVPSPKTPPEAPHVPSKTPPEAK 888
QY 72 VENAPQAEVTPPVQ-----PQSKIDGSPDKIGSVKLNKEAQTLESLRFTLVKLGTPP 126
DB 889 IPEPKTPDPVKLPDVKLPDAPKLPDGLNKVQAVFTSDGNT---KVTVV-----937
QY 127 KFDKVSCKKIEEKDFVLVNLSDINAEQLSGDFLIRSDLLFGYVYHDTGKLVDAADK 186
DB 938 -FDKPT-----DADKLHLKEVTTKELADKIA-----HKTGGTV-----970
QY 187 PSQVFFVVD-----EKRVDNISDKLTATYRKKEGPFVYVGNPHTKFAARISKLDV 238
DB 971 -----RVFDLSLKGKETHVNGERTVRLALGQTGSDVHVY---HVKE-----NGDL 1014
QY 239 E---IKFENGQAQSIKDEKGNAEIFTIKGDTYKQLEITTESNRILAILDQNKSYTP 295
DB 1015 ERIPSKVENGQV-----FKTNHFSLFAIKTSLXQDNVTPPKQT-----KPSTQ 1058
QY 296 QMEKAIMET---KFLDSKAGN 313
DB 1059 GSQVEIAESQTKF-QSKAAN 1078

RESULT 10
BAG_STRAG STANDARD; PRT; 1164 AA.
AC F27951;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IGA FC receptor precursor (Beta antigen) (B antigen).
GN Name:bag;
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=1311;
RN [1]
```

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RP SEQUENCE FROM N.A., AND SEQUENCE OF 38-48.
RC STRAIN=LA239;
RX MEDLINE=91312121; PubMed=1857207;
RA Jerslstrom P.G., Chhatwal G.S., Timmis K.N.;
RT "The Iga-binding beta antigen of the c protein complex of Group B
RT streptococci: sequence determination of its gene and detection of two
RT binding regions.";
RL Mol. Microbiol. 5:843-849(1991).
RN [2]
RP IDENTIFICATION OF IG-LIKE DOMAIN.
RX MEDLINE=97035265; PubMed=8880921;
RA Bateman A., Eddy S.R., Chothia C.;
RT "Members of the immunoglobulin superfamily in bacteria.";
RL Protein Sci. 5:1939-1942(1996).
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; X59771; CAA42442.1; -.
DR PIR; S15330; FCSOAG.
DR InterPro; IPR004829; Csurface_antigen.
DR InterPro; IPR005877; Gpos_ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR007756; RICH.
DR InterPro; IPR010989; t-snare.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF05062; RICH; 1.
DR Pfam; PF04650; Ysirk_signal; 1.
DR ProDom; PD153432; Csurface_antigen; 1.
DR TIGRfams; TIGR01167; LPXTG_anchor; 1.
DR TIGRfams; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS50835; IG LIKE; FALSE NEG.
KW Cell wall; Direct protein sequencing; Immunoglobulin domain;
KW Peptidoglycan-anchor; Receptor; Signal.
FT SIGNAL 1 37
FT CHAIN 38 1135 Iga FC receptor.
FT PROPEP 1136 1164 Removed by sortase (Potential).
FT DOMAIN 434 534 Ig-like.
FT DOMAIN 199 438 Iga-binding (Potential).
FT DOMAIN 439 826 Iga-binding (Potential).
FT DOMAIN 827 944 Pro-rich.
FT SITE 1132 1136 LPXTG sorting signal (Potential).
FT MOD_RES 1135 1135 Pentaglycyl murein peptidoglycan amidated threonine (Potential).
SQ SEQUENCE 1164 AA; 131051 MW; 65DE94AF720A5474 CRC64;

Query Match 10.0%; Score 173; DB 1; Length 1164;
Best Local Similarity 23.3%; Pred. No. 0.05;
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;

QY 12 TPNHKEVLPVKTQNNLQAQNVFQAQNASQAQNAQNAQNAQNAQNAQNAQNAQNAQ 71
DB 829 TPTDKPIPELPQADPTPQADPTHPVPSKAPAPRVPSPKTPPEAPHVPSKTPPEAK 888
QY 72 VENAPQAEVTPPVQ-----PQSKIDGSPDKIGSVKLNKEAQTLESLRFTLVKLGTPP 127
DB 889 VPESKTPPEAPHVPSPKTPPEAKIP-----EPPKTPDVKLPDVKLPDVK 936
QY 128 -----FDKVSCKKIEEKDFVLVNLSDINAEQLSGDFLIRSDLLFGYVYHDTGK 164
DB 937 LPDAPKLPDGLNKVQAVFTSDGNTKVTVDKPTDADKLHLKEVTTKELADKIA----- 992
QY 165 DDLFGYVYHDTGKLVDAADKESQVFFVVD-----EKRVDNISDKLTATYRKKEG 216
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```
Db 993 -----HKTGGTV-----RVFDSLKSGKETHWNGERTVRLALGOTGSDV 1033
QY 217 FVYGSNPHKFAARISKLDGVE---IKPENGQAQGSINKDEKGNAEIFTIKGDFKQLEI 273
Db 1034 HVY-----HVKE-----NGDLRIPSKVNGQV-----FKTNHFSFAKTKSKQNV 1077
QY 274 TPTESNRHIIAILDQNKQSYTPGMEKAIMET---KFIDSKAGN 313
Db 1078 TPKQOT-----KPTQGSQVIEAETSQTKF-QSKAAN 1108

RESULT 11
Q8TLE6 PRELIMINARY; PRT; 1443 AA.
AC Q8TLE6; MEDLINE=22092622; PubMed=12097910;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Similar to Mus musculus (Mouse). GABA-A receptor epsilon-like
DE subunit.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116960; AAM08494.2;
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
SQ SEQUENCE 1443 AA; 167562 MW; 145B36EBF31D7350 CRC64;

Query Match 9.9%; Score 172; DB 2; Length 1443;
Best Local Similarity 25.0%; Pred. No. 0.074;
Matches 82; Conservative 48; Mismatches 130; Indels 68; Gaps 12;

QY 7 GGSSTPNHPKPVLPVKTQNNLQNVPOQNASQAQNAPOAQNAPOAQNAPOAQNAPOA 66
Db 362 GFSTQALSQPTTAP-----ISFSAQSQPQ-QPQSQSQSQSQSQSQSQSQSQSQSQSQ 417
QY 67 QNAPOVENAPOAEVTPVPQSQKIDGSPKIGSVKLKEAQTLESLRFLVDKLGTPP 126
Db 418 QSQPTPSAPIGFSTQSQPQLOLQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 460
QY 127 KFDKVGSKKIEEDKFLVNLSDINASQLSGDFLIRSDDLFGYYHYDHTNGKNLVDAA 186
Db 461 KFIST-----FSQGSFNNFNNNNDIQFIELSLRSYDL-----ER 498
QY 187 FSQFVVYDEKRVNDISDKLTATYRKKEGVYSGNPHTEFAARISKLDGVSIKENGQ 246
Db 499 FKNVLL--ENKSNNDIILKVN-NHKOMGEKLGNN---IDRCFENKFKYTSNISFNMD 552
QY 247 -----AQGSIKDEKGNAEIFTIKGTQLEITPTESNRHII-----AILDQNK 292
Db 553 FDLRIQNYIFSTNQDEFNKNIEKTISSNTRELLNLLPSKWNQLLPDFTENFCLDPGKT 612
QY 293 YTPGMEKAIMETKIDSKAGNSDKYLI 320
Db 613 YF-----SIDKKETIDWIFENLKNQYFI 635

RESULT 12
Q8BMN8 PRELIMINARY; PRT; 405 AA.
AC Q8BMN8; MEDLINE=99279253; PubMed=10349636;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE enriched library, clone:5330409A03 product:weakly similar to GLUTAMINE
DE REPEAT PROTEIN-1.
GN Name=L3mbtl3; (Mouse).
OS Mus musculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary gland;
```





DR EMBL; AK129443; BAC98253.1; --  
 FT NON TER 1  
 SQ SEQUENCE 761 AA; 85935 MW; A21FF7411767346C CRC64;  
 Query Match 9.3%; Score 162; DB 2; Length 761;  
 Best Local Similarity 52.7%; Pred. No. 0.14; Mismatches 26; Indels 6; Gaps 2;  
 Matches 39; Conservative 3; Mismatches 26; Indels 6; Gaps 2;  
 QY 21 VKTQNNLQAQNV---QAQNASQAQNAFQAQNAQNAQV---ENAPQAQNAPOVEN 74  
 Db 556 VQHAQPPQAQAPQAQQAQQAQQAQAPQTPTQPQAQVQAQQAQQAQQAQQAQ 615  
 QY 75 APQAEVTPVPQPQ 88  
 Db 616 AQQPQAQPPVQPQ 629  
 RESULT 16  
 Q8BLB7 PRELIMINARY; PRT; 883 AA.  
 AC Q8BLB7;  
 DT 01-MAR-2003 (TREMELrel. 23, Created)  
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
 DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length  
 DE enriched library, clone:B230219004 product:weakly similar to GLUTAMINE  
 DE REPEAT PROTEIN-1.  
 GN Name=L3mbtl3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RA The FANTOM Consortium,  
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtration of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK045667; BAC32449.1; --  
 DR HSP; P39769; 1KW4.  
 DR MGD; MGI:2143628; L3mbtl3.  
 DR InterPro; IPR000886; ER target\_S.  
 DR InterPro; IPR004092; Mbt.  
 DR InterPro; IPR001660; SAM.  
 DR Pfam; PF02820; Mbt; 3.  
 DR Pfam; PF00536; SAM 1; 1.  
 DR SMART; SM00561; Mbt; 3.  
 DR SMART; SM00454; SAM; 1.  
 DR PROSITE; PS00014; ER TARGET; UNKNOWN\_1.  
 DR PROSITE; PS0105; SAM DOMAIN; 1.  
 SQ SEQUENCE 883 AA; 99137 MW; 7A6417202A0E5532 CRC64;  
 Query Match 9.3%; Score 162; DB 2; Length 883;  
 Best Local Similarity 52.7%; Pred. No. 0.17;  
 Matches 39; Conservative 3; Mismatches 26; Indels 6; Gaps 2;  
 QY 21 VKTQNNLQAQNV---QAQNASQAQNAFQAQNAQNAQV---ENAPQAQNAPOVEN 74  
 Db 678 VQHAQPPQAQAPQAQQAQQAQQAQAPQTPTQPQAQVQAQQAQQAQQAQQAQ 737  
 QY 75 APQAEVTPVPQPQ 88  
 Db 738 AQQPQAQPPVQPQ 751  
 RESULT 17  
 Q9RCG1 PRELIMINARY; PRT; 365 AA.  
 AC Q9RCG1;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
 DE Outer membrane lipoprotein.  
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Actinobacillus.  
 CX NCBI\_TaxID=715;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=8329;  
 RX MEDLINE=98126231; PubMed=9466755;  
 RA Gram T., Ahrens P.;  
 RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae  
 RT based on the nucleotide sequence of an outer membrane lipoprotein";  
 RL J. Clin. Microbiol. 36:443-448(1998).  
 DR EMBL; U86687; AA000620.1; --  
 DR InterPro; IPR005014; Lipoprotein\_14.  
 DR Pfam; PF03346; Lipoprotein\_14; 1.  
 KW Lipoprotein.  
 SQ SEQUENCE 365 AA; 39750 MW; E20A60DB246DAES CRC64;  
 Query Match 9.3%; Score 160.5; DB 2; Length 365;

Best Local Similarity 24.1%; Pred. No. 0.07;  
Matches 92; Conservative 54; Mismatches 139; Indels 97; Gaps 21;

QY 1 CGSGSGSSSTPNHPKPVLPVKTQNNLQAVNPQVQASQANAPQANAPQANQ 56  
Db 20 CGSGSGSSSSKPNSE---LTPKVD-----MSAPKAEQ-----PKKEVPQADNSKAE 64

QY 57 -----APOVENAQAQN-----APOVENA-----POAEVTPVPQSQKIDGSDFKIGSVK 103  
Db 65 EPKEMAPQVD-SPKAEPPKNAPOQGNPKLNDPQV-MAPKMDNPQKADPKGE-----E 115

QY 104 LNKEAQTLLESLRFTLVLDK--GTPPKPKVSGKKIIEEKDFL--VLNLSDNAEQLSGDF 159  
Db 116 LSKDKSNAEILKELGVKDINSIINNADVNLK-IDEKHITVLDKDKINRHLKVTN 174

QY 160 LIRSDDLFGYHYHDNGKLVDAADKFSQY--FVYDDEKRVNDNISDKLTATYRKKEGF 217  
Db 175 TISAQDI-----KTLKSSGKLLGYGYMQLNQVQDENYSDEKVSU---NEY 220

QY 218 VYGSNPHTEFAAR-ISKLGDEVIKFE--NGQAQGSIKDEKGNAEIETIK-----265  
Db 221 LLSMNDADKIRPTKSIYKGMFYSYKDVGNQKLKASVEASYDDATKYSKMKVFGENNDY 280

QY 266 -----GDTKOLEITPTES-----NRIIAILDQNKSYTPGMEKAIMETKFDISK 310  
Db 281 WKLGFEFRTNLENQVTKAGVGEDGTIINGLYSKIDNFKLTP-----DANFSGGI 333

QY 311 AGNSDQKYLIGKSDNQAIM 332  
Db 334 FGKNGE-VLAGSAISEKQWQVI 354

RESULT 18  
OMLA\_ACTPL STANDARD; PRT; 365 AA.

AC Q02937;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Outer membrane lipoprotein A precursor.  
GN Name=omla;  
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Actinobacillus.  
OX NCBI\_TaxID=715;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Serotype 1 / Isolate AP37;  
RX MEDLINE=93138779; PubMed=8423086;  
RA Potter A.A., Willson P.J.;  
RA Gierach G.-F., Anderson C., Klashinsky S., Rossi-Campos A.,  
RT "Molecular characterization of a protective outer membrane lipoprotein (Omla) from Actinobacillus pleuropneumoniae serotype 1.";  
RL Infect. Immun. 61:565-572(1993).  
CC 1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor.  
CC  
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CC  
CC EMBL; L06318; AAC41456.1; -;  
DR PIR; A49235; A49235.  
DR InterPro; IPR005014; Lipoprotein\_14.  
DR Pfam; PF03346; Lipoprotein\_14; 1.  
DR ProDom; PD023715; Lipoprotein\_14; 1.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Lipoprotein; Outer membrane; Palmitate; Signal.  
FT SIGNAL 1 19

FT CHAIN 20 365 Outer membrane lipoprotein A.  
FT LIPID 20 20 N-palmitoyl cysteine (Probable).  
FT LIPID 20 20 S-diacylglycerol cysteine (Probable).  
SQ SEQUENCE 365 AA; 39784 MW; 20D4B3FAEBE2842F CRC64;

Query Match 9.2%; Score 159.5; DB 1; Length 365;  
Best Local Similarity 24.1%; Pred. No. 0.081;  
Matches 92; Conservative 54; Mismatches 139; Indels 97; Gaps 21;

QY 1 CGSGSGSSSTPNHPKPVLPVKTQNNLQAVNPQVQASQANAPQANAPQANQ 56  
Db 20 CGSGSGSSSSKPNSE---LTPKVD-----MSAPKAEQ-----PKKEVPQADNSKAE 64

QY 57 -----APOVENAQAQN-----APOVENA-----POAEVTPVPQSQKIDGSDFKIGSVK 103  
Db 65 EPKEMAPQVD-SPKAEPPKNAPOQGNPKLNDPQV-MAPKMDNPQKADPKGE-----E 115

QY 104 LNKEAQTLLESLRFTLVLDK--GTPPKPKVSGKKIIEEKDFL--VLNLSDNAEQLSGDF 159  
Db 116 LSKDKSNAEILKELGVKDINSIINNADVNLK-IDEKHITVLDKDKINRHLKVTN 174

QY 160 LIRSDDLFGYHYHDNGKLVDAADKFSQY--FVYDDEKRVNDNISDKLTATYRKKEGF 217  
Db 175 TISAQDI-----KTLKSSGKLLGYGYMQLNQVQDENYSDEKVSU---NEY 220

QY 218 VYGSNPHTEFAAR-ISKLGDEVIKFE--NGQAQGSIKDEKGNAEIETIK-----265  
Db 221 LLSMNDADKIRPTKSIYKGMFYSYKDVGNQKLKASVEASYDDATKYSKMKVFGENNDY 280

QY 266 -----GDTKOLEITPTES-----NRIIAILDQNKSYTPGMEKAIMETKFDISK 310  
Db 281 WKLGFEFRTNLENQVTKAGVGEDGTIINGLYSKIDNFKLTP-----DANFSGGI 333

QY 311 AGNSDQKYLIGKSDNQAIM 332  
Db 334 FGKNGE-VLAGSAISEKQWQVI 354

RESULT 19  
Q9R3L8 PRELIMINARY; PRT; 365 AA.

ID Q9R3L8;  
AC Q9R3L8; (TREMELrel. 13, Created)  
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Outer membrane lipoprotein.  
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Actinobacillus.  
OX NCBI\_TaxID=715;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=56153, S4074, and CUI 13261;  
RX MEDLINE=98126231; PubMed=9466755;  
RA Gram T., Ahrens P.;  
RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae based on the nucleotide sequence of an outer membrane lipoprotein.";  
RL J. Clin. Microbiol. 36:443-448(1998).  
DR EMBL; U86686; AAD00619.1; -;  
DR EMBL; U86675; AAD00608.1; -;  
DR EMBL; U86684; AAD00617.1; -;  
DR InterPro; IPR005014; Lipoprotein\_14.  
DR Pfam; PF03346; Lipoprotein\_14; 1.  
KW Lipoprotein.  
SQ SEQUENCE 365 AA; 39842 MW; 5E46DFCB542781E CRC64;

Query Match 9.2%; Score 159.5; DB 2; Length 365;  
Best Local Similarity 24.1%; Pred. No. 0.081;  
Matches 92; Conservative 54; Mismatches 139; Indels 97; Gaps 21;

QY 1 CGSGSGSSSTPNHPKPVLPVKTQNNLQAVNPQVQASQANAPQANAPQANQ 56  
Db 20 CGSGSGSSSSKPNSE---LTPKVD-----MSAPKAEQ-----PKKEVPQADNSKAE 64

```

QY 57 -----APQVENAPQACN-----APQVENA-----POAEVTPVPVPOQSQIDGSPDKITGSVK 103
      : : : : :
Db 65 EPKEMAPQVD-SPKAEERPKNAPQGNPKLNDFQV-NAPKNDNPQKDAPKGE-----E 115
      : : : : :
QY 104 LNKEAQTLELSRFTLVLDKL--GTPKPKFKVSGKKIIEEKDFL--VLNLSIDINAEQLSGDF 159
      : : : : :
Db 116 LSKDSRNBAILKELGVKDINSIINNADVVLNLK-IDEKSHITVLDKOKINENHLKVTIN 174
      : : : : :
QY 160 LTRSDDLPGYYHTNGKQLVDAADKFSQY--FVVYDEKRVNDNISDKLTATYRKKEGF 217
      : : : : :
Db 175 TISAQDI-----KTLKDSGKLGYYGMQLNQRVDENYSDEKVSU--NEYV 220
      : : : : :
QY 218 VYGSNPHTKEFAAR-ISKLGDVVEIKFE---NGQAQGSIKDEKDGNAEIFTIK----- 265
      : : : : :
Db 221 LLSMNDADKIRPTKSISYKGMDFYSYKDVGNQKUKASVEASYDDVTKKYKSMKVFGCENNDY 280
      : : : : :
QY 266 -----GDRKQLEIITPES-----NRIIAILDQNKSYTPGMKXAIWETAFIDSK 310
      : : : : :
Db 281 WKLGFBGRTNLENOVTGAKYGEGBGTINGTLYSKIDNFPFLKUTP-----DANFSGGI 333
      : : : : :
QY 311 AGNSQKYLIGEAKSDNNQAIM 332
      : : : : :
Db 334 FGKNGE-VLAGSAISEKQWQVI 354
      : : : : :

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RESULT 20
P91448
ID P91448 PRELIMINARY; PRT; 896 AA.
AC P91448;
DT DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Prion-like (Q/N-rich)-domain-bearing protein protein 66.
GS Name=pqn-66; ORFNames=tl6A1.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodexinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1] RN RN
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RN RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.; Goela D.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[3] RN RN
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
EMBL; U80454; AAC3876.3; -.
DR WormPep; tl6A1.7; CE32724.
KW Prion.
SQ SEQUENCE 896 AA; 101378 MW; 3A91076B7E3346837 CRC64;

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QY	114	SRFTLVLDVLTGPPFKD---VSGKIIIEK 140
		:    :
DB	848	---GLMDLVG---GFEXHTLDVSTLKTIEK 872
		:    :
RESULT 21		
Q9RCG2		PRELIMINARY; PRT; 375 AA.
ID	Q9RCG2	
AC	Q9RCG2;	
DT	01-NAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-WAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Outer membrane lipoprotein.	
OS	Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;	
OC	Pasteurellaceae; Actinobacillus.	
OX	NCBI_TaxID=715;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=M62;	
EX	MEDLINE=98126231; PubMed=9466755;	
EX	Gram T., Ahrens P.;	
RT	"Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae	
RT	based on the nucleotide sequence of an outer membrane lipoprotein.";	
RL	J. Clin. Microbiol. 36:443-448(1998).	
DR	EMBL; U86678; AAD00611.1; -	
DR	InterPro; IPR005014; Lipoprotein_14.	
DR	Ffam; PF03346; Lipoprotein_14; I.	
KW	Lipoprotein.	
SEQUENCE	375 AA; 40840 MW; 67BAG2BE58E01A02 CRC64;	

RESULT	22
ID	O15687
AC	O15687; PRELIMINARY; PRT: 194 AA.
DT	O1-JAN-1998 (TREMBRel. 05, Created)
DD	01-JUN-1998 (TREMBRel. 05, Last sequence update)
DE	01-JUN-2003 (TREMBRel. 24, Last annotation update)
	Mexozoite surface protein 2 (Fragment).

QY	111	LELSRFTLVDLKGTTPKPKVSKKIIIEBKDFLV-LNLGSDINAEQLSGDPLIRRSDDL--	167
Db	132	KD:::KGIITRSDVLLNLTIDEGNTQIRLSESDIVENDLKITWTIPNQDIRTL	184
QY	168	---FYGYH:---DTNGKLVDAADKFSQYFVVVDEKRVNDNISDKLTATY	211
Db	185	KDSTGRLLGYGYMQLNQVREGERYGINNVDLV--CHVLLSMD--STKTAPNKSIEY	238
QY	212	RKEGFFVG-SNPHTKEFAARISKLGVEIKFENGQAQGSIKDEKDGNAEIFTIKGDTKQ	270
Db	239	RGR--MLYGYKYNDRNLVA---DVOQSYNH---SDKLSMEIFGDHGDIWK	282
QY	271	L---EITPESNRITIIALDONKSYTSGMEKAIMETKFDISKAG	312
Db	283	LGAIGNRLPKDMVTGVVDDKGTISNAGLYSKIDN----TPG--KLTPDATFSGGIFG	335
QY	313	NSDQKYLIGEAKSDNQWQAIM	332
Db	336	KNGD--VLAGSADGKNWQGI	354
RESULT 24			
QY	Q9RCG3	PRELIMINARY;	PRT; 368 AA.
AC	Q9RCG3;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Outer membrane lipoprotein.		
OS	Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;		
OC	Pasteurellaceae; Actinobacillus.		
NCBI	NCBI_TaxID=715;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=S1536;		
RX	MEDLINE=98126231; PubMed=9466755;		
RA	Gram T., Ahrens P.;		
RT	"Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae		
RT	based on the nucleotide sequence of an outer membrane lipoprotein."		
EL	J Clin. Microbiol. 36:443-448(1998).		
DR	EMBL; U86676; RAD00609.1; --		
DR	InterPro; IPR005014; Lipoprotein_14.		
DR	Pfam; PF03346; Lipoprotein_14; 1.		
KW	Lipoprotein.		
QY	Q9RCG3	SEQUENCE 368 AA; 39967 MW; 0281948BF2B8E783 CRC64;	
Query Match 8.5%; Score 147; DB 2; Length 368;			
Best Local Similarity 24.2%; Pred. No. 0.47; 139; Indels 100; Gaps 24;			
Matches 93; Conservative			
QY	1	CGSGSGSGSSSTPNHPKFLVLPVPTQNNLQCNVPQANASQAQNAPOAQN----	56
Db	20	CSGGSGSGSSSKNSE--LTPKVD-----MSAPKAEQ-----PKKEEVPQADNSKAE	64
QY	57	-----APQVENAQAQN-----APQVENA-----PQAEVTPVPQOSKIDGSPFKIGSVK	103
Db	65	EPEKMAPQVD--SPKAEPEFKMAPQMGPKLNDPQV-NAPKMDNPQKDAPKGE-----E	115
QY	104	LNKEAQTLLEISRFTLVDKL--GTPPKFDKYSKGKIIIEKD--FLVLNLSDINAPQLSGDF	159
Db	116	LSKDKSNABEILKELGVZDINSIINNADVNLK-IDEKQIKIVLDKSEINRDSLKVYN	174
QY	160	LIRASDDL-----FYGY-----HDTNKGNLVDAADKFSQYFVVYDEKR	198
Db	175	AIPTQDIKTLKSSGKLLGYGYMQLSQVRQDESYSTDSLNL-----SNYYLLSMNEQ	227
QY	199	VNDNISDKLTATYRKKEGFFVG--SNPHTKEFAARISKLGVEIKFENGQAQGSIKD----	253
Db	228	EKTRPSKSLT-----YKGTMTYIGYSSVANNKLEAEVKAQYDHSSKKLSMQVFGQNEHWRL	283
QY	254	-EKDGNAEIIFTIKGDTKQL-EITPESNRITIIALDONKSYTSGMEKAIMETKFDIS	309

Db 284 ABASG---INNVLKPSKLRDVIIVSDKGDINGLLYLEDSTPSKFTTP-----NANFSGG 333

QY 310 KAGNSDQKYLIGEAKS---DNWQAIM 332

Db 334 FFGKNGE-VLAGKAESIKGEQGV 357

RESULT 25

Q9RIH8 PRELIMINARY; PRT; 368 AA.

AC Q9RIH8; (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Outer membrane lipoprotein.

OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Actinobacillus.

OX NCBI\_TaxID=715;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=405;

RX MEDLINE=98126231; PubMed=946755;

RA Gram T., Ahrens P.;

RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae

RT based on the nucleotide sequence of an outer membrane lipoprotein.";

RL J. Clin. Microbiol. 36:443-448(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=405;

RX MEDLINE=405;

RA Gram T., Ahrens P., Angen O.;

RL Submitted (NOV-1999) to the EMBL/GenBank/DBSJ databases.

DR EMBL, U86683; AA00616.2; -

DR InterPro; IPR005014; Lipoprotein\_14.

DR Pfam; PF03346; Lipoprotein\_14; 1.

KW Lipoprotein.

SQ SEQUENCE 368 AA; 40031 MW; 9584COED96EC9A CRC64;

Query Match 8.5%; Score 147; DB 2; Length 368;

Best Local Similarity 24.2%; Pred. No. 0.47;

Matches 93; Conservative 53; Mismatches 139; Indels 100; Gaps 24;

QY 1 CGSGSGSSSTPHPKFVLVPEKTKNNLQAVQVPAQNASQAQAPQAQAPQAQON--- 56

Db 20 CSGSGSGSSSKPNSSE---LTPKVD-----MSAPKAEQ-----PKKEVPQADNSKAE 64

QY 57 -----APOVENAQAQON-----APQVENA-----PQAEVTPVPQSQKIDGSPKIGSVK 103

Db 65 EPKEVAPQVD-SPKAEPEKNAQPNQGNPKLNDPQV-WAPKNDNPKDAPKGE-----E 115

QY 104 LKKEAQTELESRFTLVDLK--GTEPKPKVSGKIIIEKD--FLVLNLSLIDNABQLSGDF 159

Db 116 LSKDKSNAEILKELGVKDGINSGLNNADVNLX-IDKQIKIVLQKSEINRDSLKVTN 174

QY 160 LIRSRDDL-----FVGY-----HDNGKVLVDAADKPFQYFVVYDEKR 198

Db 175 AIPTQDITLKDSSGKLLGYGYQMQLSQVRQDESYSYDLSLNL-----SNVYLLSMNEQ 227

QY 199 VNDNLSDLTATYRKGEFVYG-SNPHTKEFAARISKLGVDEIKFENGQAQGSIKD---- 253

Db 228 EKTRPSKSLT-----YKGTMIYGVSAVANKLEAEVKAQYDHSSKLLSNQVFGQDNEHRL 283

QY 284 -EKGNNAEIFIKGTGKOL-EITTESNRI--IIAILDQNKQSVTPGWEKAIMETKFDIS 309

Db 284 ABASG---INNVLKPSKLRDVIIVSDKGDINGLLYLEDSTPSKFTTP-----NANFSGG 333

QY 310 KAGNSDQKYLIGEAKS---DNWQAIM 332

Db 334 FFGKNGE-VLAGKAESIKGEQGV 357

RESULT 26

Q9VYV7 PRELIMINARY; PRT; 837 AA.

AC Q9VYV7; (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE CGI745-PB.

GN ORFNames=CGI745;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazell R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fesler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosher A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinart K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.X., Wasserman D.A., Weinstein G.M., Weissenbach J., Ye J.,

RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=2426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=2426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Swirskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";

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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaninkar J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt D.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
SEQUENCE FROM N.A.
RX FLYBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
RX FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003486; AAF48046.1; -.
DR IntAct; Q9VYV7; -.
DR FLYBASE; FBGN030301; CG1745.
SQ SEQUENCE 837 AA; 25296 MW; 252D9C00D649DB18 CRC64;

Query Match 8.5%; Score 147; DB 2; Length 837;
Best Local Similarity 24.4%; Pred. No. 1.3; Mismatches 126; Indels 60; Gaps 14;
Matches 77; Conservative 52;

Qy 17 KPVLPVPTQNNLQANVPQAGNQAQNAPOAQNAPOAQNAPOAQNAPOAQNAPOAQNAPOV--- 73
Db 474 KPVL--KKQDAQKKQ-PKPKLERSNKKTQMLKEKETTQKQTKKEKKTIENSPVVIIES 530

Qy 74 NAPAQAVTPVPVQPOSQKIDGSF--DKIGSVKLKKEAQTLIELSFTLVLDKLGTPPKFDKV 131
Db 531 SDPVEIKPPVKYETINEREGDAHETETNEVERDEREQVD-----ATEKNTDEA 580

Qy 132 SGKXIIIEKDFVLNLSIDINAEQLSGDFLIIRSDLFVGYVHDNGKNLVDAADKFSOYF 191
Db 581 KEKVV--KMPKLKPAD-NSEKSED---AREVLL-----DEDEKNLENAAEISDNA 629

Qy 192 VVYDEKRVNDNISDKLTATYKKEGFVYGSNPHTKFAARISKLGDVIEIKFENGQAQGS 251
Db 630 VKSLEKPTNEDRVEK-----VEDEVEHAEEFS-----DLPTP---POLPSTT 668

Qy 252 KDEKDGNAEITIKDGTKQL-----BITPTESNRILAILDQNKQSVTPGME----KAI 301
Db 669 DDNEDDVLEIQTSLDDVRQLHTPPSRQSTPKRSRLSDGSDSCFSKASDNKALLAGQAI 729

Qy 302 METKFIDSKAGNSDQ 316
Db 729 EETEQKASKAFNDDE 743

RESULT 27
Q8VSU1 PRELIMINARY; PRT; 213 AA.
AC Q8VSU1;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE C protein immunoglobulin-A-binding beta antigen (fragment).
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=90-058-4807;
RA MEDLINE=21683645; PubMed=11825981;
RA Kong F., Gowan S., Martin D., James G., Gilbert G.L.;

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RN Q6CCL1 PRELIMINARY; PRT; 1309 AA.  
AC Q6CCL1  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to sp|P08640|Saccharomyces cerevisiae YIR019c|STAI  
DE extracellular alpha-1.  
GN ORFNames=YALI0C08473g;  
OS Yarrowia lipolytica (Candida lipolytica).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Dipodascaceae; Yarrowia.  
OX NCBI\_TaxID=4952;  
(1)  
RN SEQUENCE FROM N.A.  
RC STRAIN=CLIB99;  
RG GENOLSVURES;  
RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA LaFontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boirame A., Boyer J., Catolico L., Confanioli F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hancraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenn D., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.B.;  
"Genome evolution in Yeasts."

RN Nature 430:35-44 (2004).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CLIB99;  
RA Genoscope;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
RT antigen in clinical Streptococcus agalactiae isolates are caused by  
RT genetic instability of repeating DNA sequences.";  
RL Pediatr. Res. 51:106-111(2002).  
(2)  
RN SEQUENCE FROM N.A.  
RC STRAIN=M13/99-22020;  
RA von Both U., Berner R.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY260004; AAP43682.1; -;  
DR Inter-Pro; IPR004829; Csurface\_antigen.  
DR Inter-Pro; IPR007756; RICH.  
DR Pfam; PF05062; RICH; 1.  
DR ProDom; PD153432; Csurface\_antigen; 3.  
FT NON\_TER 1  
FT NON\_TER 255  
SQ SEQUENCE 255 AA; 27495 MW; E29B5440C141970A CRC64;  
Query Match 8.0%; Score 139; DB 2; Length 255;  
Best Local Similarity 28.6%; Pred. No. 0.92; Mismatches 10; Gaps 1;  
Matches 36; Conservative 22; Indels 58; Indels 10; Gaps 1;  
QY 12 TPNHPKVLVPTKQNNLQAVPQANASQAQNAPOAQAQNAPOVENAPQAQNAPO 71  
DB 55 TPDTKIPQLPQAPDTPQAPDTHVPSPKAPAPRVPSKAPAPRVPSKAPAPR 114  
QY 72 VENAPQAEVTPVPO-----PQSKIDGSPKIGSVKLNKEAQTLELS 121  
DB 115 VPSPKAPAPRVPSKTPPEAPHVPSPKAPAPRVPSKTPPEAPHVPSPKTPPEAPK 174  
QY 122 LGTPPK 127  
DB 175 IPEPK 180  
RESULT 36  
Q6CCL1 PRELIMINARY; PRT; 1309 AA.  
AC Q6CCL1  
DT 01-OCT-2004 (TrEMBLrel. 28, Created)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to sp|P08640|Saccharomyces cerevisiae YIR019c|STAI  
DE extracellular alpha-1.  
GN ORFNames=YALI0C08473g;  
OS Yarrowia lipolytica (Candida lipolytica).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Dipodascaceae; Yarrowia.  
OX NCBI\_TaxID=4952;  
(1)  
RN SEQUENCE FROM N.A.  
RC STRAIN=CLIB99;  
RG GENOLSVURES;  
RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA LaFontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boirame A., Boyer J., Catolico L., Confanioli F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hancraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenn D., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.B.;  
"Genome evolution in Yeasts."



Mon Dec 20 08:54:29 2004

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OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13039;
RX MEDLINE=98126231; PubMed=9466755;
RA Gram T., Ahrens P.;
RT "Improved diagnostic PCR assay for Actinobacillus pleuropneumoniae
RL based on the nucleotide sequence of an outer membrane lipoprotein.";
RL J. Clin. Microbiol. 36:443-448(1998).
DR EMBL; U86685; AAD00618.1;
DR InterPro; IPR005014; Lipoprotein_14.
DR Pfam; PF03346; Lipoprotein_14; 1.
KW Lipoprotein.
SQ SEQUENCE 367 AA; 40186 MW; 53653BEA98BDEA3 CRC64;

Query Match      8.0%; Score 138.5; DB 2; Length 367;
Best Local Similarity 22.1%; Pred. No. 1.5;
Matches 91; Conservative 61; Mismatches 105; Indels 155; Gaps 26;

QY 1 CGSGSGSSSTNHPKPLVLPKTONLQANVPQANASQANAPQANQ-----APQAN 56
Db 20 CSGSGSGSSPKPNSES---TPKVDMSAPKAEPPKKEAPQA-DSPKAEKPSIAPLMWE 75
QY 57 APOVENAPQANAPQVENAPQA---EVTTP---VPOFSQKIDGSPDK----- 98
Db 76 NPKVEK--QKENNLQ-EKSPKADPEQVMDPKLGAPQKDDQKLEEPKKNKNAEILKELGIK 132
QY 99 -----IGSVKLNKEAQTLELSRTLV-----DKLGTTPKPKDKVSGKKIIEEKD--- 141
Db 133 DITSGTISIDIELNLQLDSNDNVKISLLNENLMDNLTN---NKIAGSDIRTLKDSG 189
QY 142 -----FLVLN-----LSDINAEQLSGDFLIRRSDDLFGYYH 173
Db 190 RLIGYGVQVQNVQTSRDPDNKYHQFENHYLLSMNDAEKILPEKSLVKGSMIYG-- 247
QY 174 DTRGNLVDAAKFSQYVYVYDEKRVNDNISDKLTATYRKKEGVYGSNPHYKEFAARIS 233
Db 248 NTSG-----NEKLTAEVNAK-----YDSS--TKLSMKVY 275
QY 234 -----KLGDV---EIKFENGQAGSTKDEKDG--NAEIFTIKGDTKQLEITPTESNRII 282
Db 276 DNDRYWKLGEVGNVNNVLPKPEKVDG-VKVDSDGTINARLYL--STEEPLKLT----- 325
QY 283 IAILDQNKSYTPGMERKALMETKPIDSKAGNSDQKYLIGEAKS--DNWQAIM 332
Db 326 ----DAN---FSGG-----IFGKNG-----EVLAKAESIKGEWQGV 356
```

Search completed: December 17, 2004, 16:01:41  
Job time : 225.711 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 15:52:32 ; Search time 44.3421 Seconds  
(without alignments)  
731.247 Million cell updates/sec

Title: US-10-696-544-2

Perfect score: 1734

Sequence: 1 CGSGSGSGSSITPNHPKPV.....YLIGBAKSDNQAIWVSEKK 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	177	10.2	1164	1 FCSOAG	IgA Fc receptor pr
2	173	10.0	1134	1 A60234	IgA Fc receptor pr
3	159.5	9.2	365	2 A49235	outer membrane lip
4	159.5	9.2	436	2 C88065	protein T16A1.6 [i
5	141	8.1	3164	1 WMSR6	UL36 protein - hum
6	138.5	8.0	367	2 I39649	lipoprotein - Acti
7	135.5	7.8	785	2 H90547	lipoprotein [impor
8	131	7.6	367	1 OZZQMY	circumsporozoite p
9	127	7.3	1084	2 B64088	hemoglobin-binding
10	126.5	7.3	849	2 S61962	probable membrane
11	126.5	7.3	4152	2 T31102	filamentous hemagg
12	126.5	7.3	4919	2 T31105	hypothetical prote
13	126	7.3	631	2 S70910	transferrin-bindin
14	125.5	7.2	1036	2 S73601	protein P200 - Myc
15	122.5	7.1	1010	2 T13167	Lola-like protein
16	122	7.0	599	1 A64235	cytochrome-acces
17	121	7.0	1306	2 S22624	aggregation protei
18	120	6.9	604	2 D90523	lipoprotein [impor
19	119	6.9	773	2 F90537	lipoprotein [impor
20	118.5	6.8	782	2 A82940	hypothetical prote
21	117	6.7	395	2 JC5975	aurora-related kin
22	116.5	6.7	298	2 H64625	type I restriction
23	116	6.7	488	2 B91003	transferrin-bindin
24	115.5	6.7	682	2 F30603	vipe-like [mycopla
25	115	6.6	237	2 S46984	microfilarial shea
26	113.5	6.5	375	2 T08134	oleosin-like prote
27	113	6.5	791	2 C82940	hypothetical prote
28	112.5	6.5	430	2 JC2301	hypothetical 47.8k
29	111.5	6.4	366	2 T26449	hypothetical prote

conserved hypothet  
cylidin I - human  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable membrane  
probable membrane  
hypothetical prote  
hypothetical prote  
X-linked PEST-cont  
RNA-binding protei  
ORF MSV230 hypothe  
protein R52.2 (imp  
FntB protein [impo  
aurora-related kin  
serine-repeat anti

#### ALIGNMENTS

##### RESULT 1

PCSOAG  
IgA Fc receptor precursor - Streptococcus agalactiae

N:Alternate names: beta antigen

C:Species: Streptococcus agalactiae

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C:Accession: S15330; S20240; S17038

R:Jernstroem, P.G.; Chhatwal, G.S.; Timmis, K.N.

Mol. Microbiol. 5, 843-849, 1991

A:Title: The IgA-binding beta antigen of the c protein complex of Group B streptococci

A:Reference number: S15330; MUID:9131212; PMID:1857207

A:Accession: S15330

A:Molecule type: DNA

A:Residues: 1-1164 <JER1>

A:Cross-references: UNIPROT:P27951; EMBL:X59771

A:Accession: S20240

A:Molecule type: protein

A:Residues: 38-48 <JE2>

R:Jernstroem, P.G.

submitted to the EMBL Data Library, August 1991

A:Reference number: S17038

A:Accession: S17038

A:Molecule type: DNA

A:Residues: 1-914, E', 916-1164 <JE3>

A:Cross-references: EMBL:X59771; NID:946522; PID:946523

C:Superfamily: IGA Fc receptor

C:Keywords: Cell wall; immunoglobulin receptor; tandem repeat; transmembrane protein

F:1-37/Domain: signal sequence #status predicted <SIG>

F:38-1164/Product: IGA Fc receptor #status experimental <MAT>

F:199-438/Domain: IGA binding #status predicted <IGAL>

F:439-825/Domain: IGA binding #status predicted <IGR2>

F:827-945/Region: proline-rich repeats

F:946-1131/Domain: cell wall-spanning #status predicted <CWS>

F:1132-1159/Domain: transmembrane #status predicted <TM>

Query Match 10.2%; Score 177; DB 1; Length 1164;

Best Local Similarity 23.6%; Pred. No. 0, 0023;

Matches 81; Conservative 44; Mismatches 114; Indels 104; Gaps 15;

QY 12 TENHPKPVLPVPTQNNLQAVPQASQANPQAQNAPOQNAPOQNAPOQNAPOQNAPOQ 71

DB 829 TDTTKIPQLPQADTPQADTPHVPSPKAPAPRVPSPKTPPEAPHPVSPKAPAPR 888

QY 72 VENAFAQEVTPVPQ-----PQSQKIDGDFDKIGSVKLNKEAQTLSRFTLVDKLTGTPPK 127

DB 889 VPESKTPPEAPHPVSPKTPPEAPKIP-----KPKPTDPVKLPDVPKLPDVPK 936

QY 128 -----FDKVS GK---KIIEEK--DFLVLNLSIDINAEQLSGDFLIRS 164

DB 937 LPDAPKLPGLKNKVGCAVFTSDGNTKTVVFDKTDADKHLKEVTTKELADKIA---- 992

QY 165 DDLFYGYHDTNGKNLVDAADKFSQVYVVD-----EKVNDNISDKLTATYRKKEG 216

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Db      993 -----HKTGGGV-----RVFSLSKGKETHVNGERTVRLALQGTGSDV 1033
QY      217 FYGNSPHTKFAARISKLGDVE---IKFNGQAQGSIKDEKGNABEFTIKGTQKLEI 273
Db      1034 HVY-----HVKE-----NGDLRIPSKVNGQVV-----FKTNHFSLFAIKTLSKQNV 1077
QY      274 IPTESNRIIILDONQKSYTPGMEKAIMET---KFIDSKAGN 313
Db      1078 TPKQT-----KSTQGSQVEIAESQTGKF-QSKAAN 1108

RESULT 2
A60234
I:GA Fc receptor precursor - Streptococcus agalactiae (strain SB35)
N:Alternate names: IGA-binding protein; protein Bac
N:Contains: beta antigen
C:Species: Streptococcus agalactiae
C:Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 09-Jul-2004
C:Accession: A60234; S14595; A60230
R:Heden, L.O.; Frithz, E.; Lindahl, G.
Eur. J. Immunol. 21, 1481-1490, 1991
A:Title: Molecular characterization of an Iga receptor from group B streptococci: sequen
ents with IGA-binding capacity.
A:Reference number: A60234; MUID:91257158; PMID:2044657
A:Accession: A60234
A:Molecule type: DNA
A:Residues: 1-1134 <HED>
A:Cross-references: UNIPROT:Q99051; EMBL:X58470; NID:G46520; PID:CAA41384.1; PID:G46521
A>Note: the source is designated as Group B streptococcus strain SB35
R:Heden, L.; Frithz, E.; Lindahl, G.
Submitted to the EMBL Data Library, March 1991
A:Description: Molecular characterization of an Iga receptor from group B streptococci:
fragments.
A:Reference number: S14595
A:Accession: S14595
A:Molecule type: DNA
A:Residues: 1-1134 <HE2>
A:Cross-references: EMBL:X58470; NID:G46520; PID:CAA41384.1; PID:G46521
A>Note: the source is designated as Streptococcus agalactiae
R:Lindahl, G.; Akerstrom, B.; Vaerman, J.P.; Stenberg, L.
Eur. J. Immunol. 20, 2241-2247, 1990
A:Title: Characterization of an Iga receptor from group B streptococci: specificity for
A:Reference number: A60230; MUID:91055597; PMID:2242758
A:Accession: A60230
A:Molecule type: protein
A:Residues: 'X', 39-48, 'X', 50-52, 'X', 54-56 <LIN>
A:Superfamily: IGA Fc receptor
C:Keywords: cell wall; immunoglobulin receptor; tandem repeat; transmembrane protein
F:1-37/Domain: signal sequence #status predicted <Sig>
F:38-1134/Product: IGA Fc receptor #status experimental <MAT>
F:193-438/Domain: IGA binding #status predicted <IGAL>
F:439-826/Domain: IGA binding #status predicted <IGAL>
F:827-915/Region: proline-rich repeats
F:916-1101/Domain: cell wall-spanning #status predicted <CWS>
F:1102-1129/Domain: transmembrane #status predicted <TM>

Query Match 10.0%; Score 173; DB 2; Length 1134;
Best Local Similarity 23.7%; Pred. No. 0.004;
Matches 76; Conservative 45; Mismatches 110; Indels 90; Gaps 15;

QY      12 TPNHPKPVLPKTONNLQANVPOAQNASQAQAPQAQAPQAPQAPQAPQAPQAPQ 71
Db      829 TPTPKIPELPQADPTQADPTHVPSRPAPAPVPSPKTPPEAPHVPSPKTPPEAPK 888
QY      72 VENAPAEVTPPVQ-----FQSQKIDGSPDKIG-SVKLNKEAQTLSRFTLVKLGTFP 126
Db      889 IPEPKTPDVKPLDPVPLDAPKLPDGLNKVGOAVFTSDGNT----KVTVV----- 937
QY      127 KFDKVGSKKIEEKDFVLNLSDINAEQLSGDFLIRSDDLFYGYVHDYNGKLVDAAPK 186
Db      938 -FKPT-----DADKLHLKEVTTKELADKTA-----HKTGGGV----- 970

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QY      187 FSOYFVYD-----EKRVNDNISDKLTATYRKKEGFVYGSNPHTKFAARISKLGDV 238
Db      971 -----RVFSLSKGKETHVNGERTVRLALQGTGSDVHVY-----HVKE-----NGDL 1014
QY      239 E---IKFNGQAQGSIKDEKGNABEFTIKGTQKLEITPTESNRIIILDONQKSYTP 295
Db      1015 ERIPSKVNGQVV-----FKTNHFSLFAIKTLSKQNVTPPKQT-----KPSTQ 1058
QY      296 GMEKAIMET---KFIDSKAGN 313
Db      1059 GSQVEIAESQTGKF-QSKAAN 1078

RESULT 3
A49235
outer membrane lipoprotein OmlA - Actinobacillus pleuropneumoniae
C:Species: Actinobacillus pleuropneumoniae
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49235
R:Gerlach, G.F.; Anderson, C.; Klashinsky, S.; Rossi-Campos, A.; Potter, A.A.; Willson, I.
Infect. Immun. 61, 565-572, 1993
A:Title: Molecular characterization of a protective outer membrane lipoprotein (OmlA) fr
A:Reference number: A49235; MUID:93138779; PMID:8423086
A:Accession: A49235
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-365 <GER>
A:Cross-references: UNIPROT:Q02937
A:Experimental source: serotype 1
A>Note: sequence extracted from NCBI backbone (NCBIN:123233, NCBI:P:123234)

Query Match 9.2%; Score 159.5; DB 2; Length 365;
Best Local Similarity 24.1%; Pred. No. 0.0065;
Matches 92; Conservative 54; Mismatches 139; Indels 97; Gaps 21;

QY      1 CGSGSGSGSSSTPNHPKPVLPKTONNLQANVPOAQNASQAQAPQAQAPQAPQAPQ 56
Db      20 CSGSGSGSGSSSKPNSL---LTPKVD-----MSAPKAEQ-----PKKEEVPOADNSKAE 64
QY      57 -----APOVENAPOAQN---APOVENA---POAEVTPPVPOQSQKIDGSPDKIGSVK 103
Db      65 EPKENAPQVD-SPKAEENAPQNGNPKLNDPQV-MAPQMDNFQKAPKE-----E 115
QY      104 LNKEAQTLELRFTLVKXL---GTFPKFDKVGSKKIIIEKDFL---VLNLSDINAEQLSGDF 159
Db      116 LSKDKSNAEILKELGVKQDINSIINNADVNLK-IDEKDHITVVDLKGKLNRLKVTN 174
QY      160 LIRRSDDILFYGYHDYNGKLVDAADKFSQY--FWYDEKAVNDNISDKLTATYRKKEGF 217
Db      175 TISAQDI-----KTLKSSGKLLGYGYMQLNQVQDENYSDERKVS---NEY 220
QY      218 VYGSNPHTKFAAR-ISKLGDVEIKFE---NGQAQGSIKDEKGNABEFTIK----- 265
Db      221 LLSMNDADKIRPTKSIYKGMDFYSYKDVGNQKLKASVEASVDDVTYKVSXKVGENDY 280
QY      266 -----GDTKOLEITPTES-----NRIIILDONQKSYTPGMEKAIMETKPIDSK 310
Db      281 WKLGFGFRTNLENQVTKGVGEGDTGTINGTLYSKIDNFPKLKTP-----DANFSGGI 333
QY      311 AGNSDKVYLIGEAKSDNWQAIM 332
Db      334 FKKNGE-VLAGSAISEKWQGV 354

RESULT 4
C88065
protein T16A1.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: C88065
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

```







QY 55 ---QNAPOVENAQAQNAPOVENAQAQVTPVPVPOQSQIDGSPKIGSVKLNKEAQTLL 111  
Db 121 TFPNVAPLYNA--TGPAPVNGQP-----PPPGIESQWKYIDNSNGNIQPGFOTNNMSQY 174  
QY 112 ELSRFT---LVDKLGTPPKPKDKYSGKKI-IEEKDFVLNLSDINAEQLSGDFLIRR----- 163  
Db 175 QGGYFTPTLQICHLATSPBPVNDPFRILGELTILVNNYQD---PFVAFDRIVIRALNA 231  
QY 164 -----SDDLIFY-----GYVHDT-----NGKNL 180  
Db 232 VPLVAPTSSKQKQVESRDLPFVADVHSDDPTEYEEILGLKFEDGSSYHETQVWVPVDGRHI 291  
QY 181 --VDAADKFSQYFVWYDEKRVNDNISDKLTATYRKKEGFYVGNPHTKFAARISKLGDV 238  
Db 292 TKVDTPKISAYTAPIS---TTSRGNKTTSSHEKV-----PSHBEASPE-----RQ 336  
QY 239 EIKFNGQAQSGIKDEKQGNAEFTIKGDTQKLEI---TPTESN-----RI 281  
Db 337 EVFSEEGRTVSNITNEES-----IVKNPTKQEEESRGEKEQNILDQVQPEIEEDVRKD 391  
QY 282 IIAILDQNKSYTPGM-----EKALMETKPIDSKAGNSDKYLGIEAKSDNWAQIM 332  
Db 392 VISTADEPKSKDTPQMTSEQKRFAXAELMAQKLLBEQQRQBEK-----KRRBEQRKL 445  
QY 333 VSEKK 337  
Db 446 KKEKK 450  
RESULT 11  
T31102  
filamentous hemagglutinin 1 - Haemophilus ducreyi  
C:Species: Haemophilus ducreyi  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31102  
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.  
J. Bacteriol. 180, 6013-6022, 1998  
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.  
A:Reference number: 220984; MUID:99030326; PMID:9811662  
A:Accession: T31102  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-4152 <WAR>  
A:Cross-references: UNIPROT:Q9ZHL3; EMBL:AF057695; NID:G3929017; PID:G3929018; PIDN:AAC7  
C:Genetics:  
A:Gene: lspa1  
Query Match 7.3%; Score 126.5; DB 2; Length 4152;  
Best Local Similarity 21.4%; Pred. No. 18;  
Matches 82; Conservative 61; Mismatches 130; Indels 111; Gaps 19;  
QY 13 PNHKPKVLVPTQNNLQAQNVPOAQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQV 72  
Db 2580 PEDAPPALPRTQSLIDSTEVSYSALANVKFDDASWPQ-----PSALRSKAF 2629  
QY 73 ENAPOAEVTP-----PVPOQSQKI---DGSPDKIGSVKLNKEAQTLELSR 115  
Db 2630 ADEPSE--TPKSRGKRGISEESLSSTVQPRSRKISEEDSSFERLPLRIIDNGSDYAEILP 2688  
QY 116 FTLVDKLGTPPKPKDKYSGKKIIEKDFVLNLSDINAEQLSGDFLIRRSD---LFVGY 172  
Db 2689 RNV--KQTNPEPATQAIRAPALDN-----NDVIAERPS--FKRLQDDDDVESVNGIY 2736  
QY 173 HDINGKNLVDAADKFS-QYFVVYDEKRVND-----NISDKLTATYRKKEGFVY 219  
Db 2737 SSIKPKALIEBETPIRQVKTQVETPTDLVNKRELKVEDRSLLDKVQDTF----- 2788  
QY 220 GSNPHTEFAARISKLGDV-----EIKFNGQAQSGIKDEKQGNAEFTIKGDTKQ 270  
Db 2789 -----QPLKVR-SKINDVRSSVEEYGGVTFKYAQSGEVYNEIVKHAE-----TQN 2834  
QY 271 LEITPTESNRITAILDQN-----QKSYTPGMEKAIME-----TKFIDSKAGNSD 315

Db 2835 GVCATCSHWIAKKNVDNIWTDLYKDGQGRKGLNKDAIESIEKLTQTEFIN--AGTAT 2892  
QY 316 QKYLIGEAKSDNW---QAIMVSEK 336  
Db 2893 QQFKL-----TNTWLEEGQVVPKQK 2912  
RESULT 12  
T31105  
hypotheetical protein 2 - Haemophilus ducreyi  
C:Species: Haemophilus ducreyi  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31105  
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.  
J. Bacteriol. 180, 6013-6022, 1998  
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.  
A:Reference number: 220984; MUID:99030326; PMID:9811662  
A:Accession: T31105  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-4919 <WAR>  
A:Cross-references: UNIPROT:Q9ZHL0; EMBL:AF057696; NID:G3929021; PID:G3929023; PIDN:AAC7  
C:Genetics:  
A:Gene: lspa2  
Query Match 7.3%; Score 126.5; DB 2; Length 4919;  
Best Local Similarity 21.4%; Pred. No. 22;  
Matches 82; Conservative 61; Mismatches 130; Indels 111; Gaps 19;  
QY 13 PNHKPKVLVPTQNNLQAQNVPOAQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQV 72  
Db 2709 PEDAPPALPRTQSLIDSTEVSYSALANVKFDDASWPQ-----PSALRSKAF 2759  
QY 73 ENAPOAEVTP-----PVPOQSQKI---DGSPDKIGSVKLNKEAQTLELSR 115  
Db 2759 ADEPSE--TPKSRGKRGISEESLSSTVQPRSRKISEEDSSFERLPLRIIDNGSDYAEILP 2817  
QY 116 FTLVDKLGTPPKPKDKYSGKKIIEKDFVLNLSDINAEQLSGDFLIRRSD---LFVGY 172  
Db 2818 RNV--KQTNPEPATQAIRAPALDN-----NDVIAERPS--FKRLQDDDDVESVNGIY 2865  
QY 173 HDINGKNLVDAADKFS-QYFVVYDEKRVND-----NISDKLTATYRKKEGFVY 219  
Db 2866 SSIKPKALIEBETPIRQVKTQVETPTDLVNKRELKVEDRSLLDKVQDTF----- 2917  
QY 220 GSNPHTEFAARISKLGDV-----EIKFNGQAQSGIKDEKQGNAEFTIKGDTKQ 270  
Db 2918 -----QPLKVR-SKINDVRSSVEEYGGVTFKYAQSGEVYNEIVKHAE-----TQN 2963  
QY 271 LEITPTESNRITAILDQN-----QKSYTPGMEKAIME-----TKFIDSKAGNSD 315  
Db 2964 GVCATCSHWIAKKNVDNIWTDLYKDGQGRKGLNKDAIESIEKLTQTEFIN--AGTAT 3021  
QY 316 QKYLIGEAKSDNW---QAIMVSEK 336  
Db 3022 QQFKL-----TNTWLEEGQVVPKQK 3041  
RESULT 13  
S70910  
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB32)  
C:Species: Haemophilus influenzae  
A:Variety: strain SB32  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S70910; S73323  
R:Liocomore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.  
Mol. Microbiol. 19, 575-586, 1996  
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes.  
A:Reference number: S70901; MUID:96228706; PMID:8830248  
A:Accession: S70910  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA

A;Residues: 1-631 <LOO>  
A;Cross-references: UNIPROT:Q48043; EMBL:U15057  
A;Experimental source: strain SB32, clone DS-1047-4-10  
R;Loosemore, S.M.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S73320  
A;Accession: S73323  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-241, 'P', 243-420, 'C', 422-508, 'A', 510-631 <LOW>  
A;Cross-references: EMBL:U15057; NID:g1223952; PIDN:AAC43933.1; PID:g1223953  
A;Experimental source: strain SB32, clone DS-1047-4-10  
C;Genetics:  
A;Gene: cbp2  
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 7.3%; Score 126; DB 2; Length 631;  
Best Local Similarity 24.0%; Pred. No. 1.7; Mismatches 45; Indels 70; Gaps 14;  
Matches 67; Conservative 45; Mismatches 45; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPPVFPQ-----SQIDGSPDKIGSVKLNKEAQTLELSRFTLVKDL 122  
Db 322 VFSAKETEKPPLKRETLIDGLTKTTFSKTTDTTNTKITSKNTTE-----NFTTKD-- 372

QY 123 GTPPKFDKVSKKIIEKDFLVNLSDINAEQLSGDFLIERSDDLFGYVYHDTNGKL-V 181  
Db 373 --IPSFG-----EADYLLIDNPPLPESGDFISSK-----HHEVGGKRYK 413

QY 182 DAADK---FSQYFVVYDVKRVNDISDK-----LTATYRKKEGFGVYGSNPHTKFEFAARIS 233  
Db 414 EACCKNLVYVFGMYEDKNNKNETDKKEKQTTTSIKYVQLGLRTPSSE---IP 469

QY 234 KLGDEVIKFGNQAGSINKDKGNNAEFTTKGDKOLEITPTESNRILIIAILDONOKSY 293  
Db 470 KMGNTYR---GSMFGYIGDKTS---YSATGDKRQDKNAPAEFN-----VDFNNKKL 516

QY 294 TPGVEKAIMETKFTIDSKA---GNSDKYLLIGEAASDNW 328  
Db 517 TGTSKRHDQNPVFNKATFQNGRNDPE---GTATAENP 552

RESULT 14  
S73601  
protein P200 - Mycoplasma pneumoniae (strain ATCC 29342)  
N;Alternate names: cyradherence-accessory protein (hmw1) homolog; hypothetical protein P  
C;Species: Mycoplasma pneumoniae  
A;Variety: ATCC 29342  
C;Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
A;Accession: S73601; S49062  
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
A;Reference number: S73327; MUID:97105885; PMID:8948633  
A;Accession: S73601  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1036 <HIM>  
A;Cross-references: UNIPROT:P75211; EMBL:AE000027; GB:U00089; NID:g1673941; PIDN:AAB9592  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
R;Proft, T.; Herrmann, R.  
Mol. Microbiol. 13, 337-348, 1994  
A;Title: Identification and characterization of hitherto unknown Mycoplasma pneumoniae  
A;Reference number: S49059; MUID:95075318; PMID:7984111  
A;Accession: S49062  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: P, 642-678 <PRO>  
A;Cross-references: EMBL:Z32646; NID:g474071; PIDN:CAA83569.1; PID:e104325; PID:g1333782  
A;Experimental source: clone D2-1C-Alu  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994  
C;Genetics:

A;Genetic code: SGC3

Query Match 7.2%; Score 125.5; DB 2; Length 1036;  
Best Local Similarity 20.2%; Pred. No. 3.4;  
Matches 77; Conservative 65; Mismatches 123; Indels 117; Gaps 20;

QY 9 SSSPTN-HPKPVLPVKTQNNLQAQNVPOAQNASQAQNAPOAQNAPQAQNAQVNAPOAQA 67  
Db 703 TESDFSEFEVEIQEPPEPFNDELTIPEPESITTE--PEPNFEVEFELEIENPFESE 760

QY 68 NAOQVENAPQAEV-TPVPV-----OPQSO---KIDGSPDKIGSVKLNKEAQT----- 110  
Db 761 TEVQQLAQESSFESEPFEPFETEVQVQSEIESKFEAEVQSEPKVSLNSDFETKPEAQ 820

QY 111 LELSFTL-VKLGTPPKFD-KVSGKKIIEKDFLVNLSDINAEQLSGDFLIERSDDLFG 168  
Db 821 ABEVTPETLEATSEAPQLPTEATKVVD-----DVEEBQLDWELLIGNSN--- 867

QY 169 YGYXH-----DTNGKLVDAADKFSQYFVVYDEKRVNDNISDKLTATY-RKKEG 216  
Db 868 YGHIYPSGEVWAGYVDDNQIWPDPASVEWAR-----ESDYTLIDGIEIYGRYNRKGEW 921

QY 217 FVYGSNPHTKFE-----ARISK-----LG-----DVEIKFENGQAQGS 250  
Db 922 IWGYVDETGEVNLVDEHYQNHQPRISEAPRFWEQLIGNEDYGYVEDNENKWDGEF--- 978

QY 251 IKDEKGNNAEFTIKG--DTKOLEITPTESNRILIIAILDONOKSYTPGWKAIMETKFD 308  
Db 979 ---DSEGNLVFHSNABDAKNIDI-----AKDIPVFESPDVD 1013

QY 309 S-----KAGNSDKYLLIGE 322  
Db 1014 SIDADEWLDDQFSDSDAKEVFG 1035

RESULT 15  
T13167  
Lola-like protein - fruit fly (Drosophila hydei)  
C;Species: Drosophila hydei  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: T13167  
R;Cavarec, L.; Jensen, S.; Casella, J.P.; Cristescu, S.A.; Heidmann, T.  
Mol. Cell. Biol. 17, 482-494, 1997  
A;Title: Molecular cloning and characterization of a transcription factor for the copia  
A;Reference number: Z17624; MUID:97127405; PMID:8972229  
A;Accession: T13167  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1010 <CAV>  
A;Cross-references: UNIPROT:O18346; EMBL:Y14994; NID:g2467111; PIDN:CAA75228.1; PID:g2467  
C;Genetics:  
F;18-119/Domain: POZ domain homology <POZ>

Query Match 7.1%; Score 122.5; DB 2; Length 1010;  
Best Local Similarity 21.9%; Pred. No. 5.1;  
Matches 70; Conservative 47; Mismatches 118; Indels 85; Gaps 14;

QY 1 CGSGSGSGSSSTPNHPKPVLPVKTQNNLQAQNVPOAQNASQAQNAPOAQNAPQAQNAPOV 60  
Db 257 CGSSSGSGSQTNQ-----PLTSSSSSSNNVTKTESAKLTSTAAAGGAQGGGQQQQQ 309

QY 61 ENAPQAQNAQVENAPQAEVTPPVQPSQKIDGSDFKI-----GSVKLNKEAQT 111  
Db 310 QTTSDAINTNVQQ-----QQNQGAQGADEMDVASGGAASGAYVHPGV--- 355

QY 112 ELSRFTLVKLGTPPKF-DKVSQKKIIEK-----DFVLNLSDINAEQL--- 155  
Db 356 -VKQUTTLIDKSNHKKIKNIDITTEWIEPKAEYDDDAHDENVEDLTLDEEDTWELDQ 414

QY 156 -----SGDFLI-----RRSDDLFGYVYHDTNGKLVDA-ADKFSQYFVVYDEKRV 199  
Db 415 AAGTSQGGGSGSSQAYATWQHDSRSDQLGLMAAQQAQRDPQDAKQDKGEQTEGAHDFEL 474

A;Gene: aspl  
A;Genome: plasmid pPd1  
C;Superfamily: aggregation protein asal

Query Match 7.0%; Score 121; DB 2; Length 1306;  
Best Local Similarity 19.7%; Pred. No. 8.9;  
Matches 87; Conservative 58; Mismatches 154; Indels 142; Gaps 19;

QY 3 GSGSGSSSTPN-----HPKVLVPKTONNL--QAQNVPAQN-ASQAQ 43  
DB 97 GIAEQSSATPNDTTNVQPTVGAESAQEQPVVSPETTNEPLGQPTVAPAEANEANKST 156  
QY 44 NAPAQAQNAPOAQNAPQVNAPOAQNAPQVENAP-----QAQVTP 82  
DB 157 TIPKEFETPDVKA--VDEAKDPNITVVEKPTEDLGNVSSKDLVEKEKEVDQLQKEQAK 214  
QY 83 PVPQSQKIDGDFDKIGSV-----KLNKAQATLELSRF----- 116  
DB 215 KIAQ-QAAELKANEXKIAENAEIAAKNKAERKEVEKAEYKHNKNDKGVNEAISKDL 273  
QY 117 ----TLVDKLGTPPKPKVSGKKIIBEKDFVLNLSLINAQLSGDFLIIRSDDLFYGY 172  
DB 274 VFDSSIVTK---DTKIDKITGGRFIKASEFNKNQG-----QSKDIFTKLS 316  
QY 173 HDYNGKNLVD-----AADKFSQ---YFVYVDEKRVNDNIDSKLTATY--RK--KEGFVY 219  
DB 317 KDMNGKATGNFQSGSKVAAEVFPKGGYAVLLEKNKPNANVTYTGNAASYLARKITKTBEFIY 376  
QY 220 GSNPHTKFAARTSKLGDVEIKFENGQAQGSIKDEKDGNAE----IFTIK-GDTKQLEIT 274  
DB 377 -----ELQSAFSQGTNLNAVESNDPIITAFVGTQWANGKDVKVRLTIKLYDANGKEVL 429  
QY 275 PTESNRIRIIAILPQNCQKSYTPGMEAKMETKFDISKAGNSDQKYLIGE----- 322  
DB 430 PERDHAFAYALSLSN---SLGTNYSVEHAEBFVSDFGSKNAFYINGSYVKKQADGKFYS 486  
QY 323 -----AKSDNQWQAI 331  
DB 487 TEDLDYGTGSLGKNSDWDV 507

RESULT 18  
D90523  
lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
C;Species: Mycoplasma pulmonis  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: D90523  
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Mo  
Nucleic Acids Res. 29, 2145-2153, 2001  
A;Title: The complete genome sequence of the murine respiratory pathogen Mycop  
A;Reference number: A99512; MUID:21267165; PMID:11353084  
A;Accession: D90523  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-604 <KUR>  
A;Cross-references: UNIPROT:Q98R37; GB:AL445566; PID:g14089505; PIDN:CAC13265.1  
A;Experimental source: strain UAB CTIP  
C;Genetics:  
A;Gene: MYPU 0920  
A;Genetic code: SGC3

Query Match 6.9%; Score 120; DB 2; Length 604;  
Best Local Similarity 19.1%; Pred. No. 3.8;  
Matches 82; Conservative 65; Mismatches 131; Indels 152; Gaps 22

QY 16 PKFVLVPKTONLQAQNVPAQNASQAQNAPOAQN-APQAQNAQ---VENAPQAQNAQ 71  
DB 58 KPAPKAPGDN--KQPTPKTPPESEKPPAPKPEGSKQPEEPTBEKQDMKNPQKPEPE 115  
QY 72 VENAPOAEVTPVPQPSQKIDGDFDKIGSVKLNKAQTLLEL-----SFTLVD 120  
DB 116 VPKAPE----PEKAPFNWVEGE-AQVELLSLSDGSLSKFKDLPENLSKLT-L-K 169



```
Best Local Similarity 25.7%; Pred. No. 3.4; Mismatches 116; Indels 48; Gaps 11;
Matches 66; Conservative 27;

QY 10 SSTNHPKPVLPK--TQNNLQANVPQQA---SQAQAP--QAQAPQAQAPQVANA 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 15 TTVPFGPKVLTVEQIPSNGLSASSQAQVLPSPNSQVPSQAQKLQAGQKPAKPKQL 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 PQQAPQVE--NAPQAEVTPVPQSQKIDGSPKIGSVKLNKAQLELSRFTLVDK 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 PAASVPRPVSRLNPNQKNEQPAASGNDSEKQASLQKTEDTK--KQWTLT--DFDIGRP 130
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 LGTPPKFDKVSQKGIIEEDFLVNL--LSDINAEQLSGDFLIRSDDL-----FY 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 LG-KGFGVNLAREQSKFIALKVLFKTQLEKANVEHQLEREVIEQSHLRHPNLTILRY 189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 170 GYHDYDNGKVLDAADKFSQYFVYDEKRVNDNISDKLTATY-----211
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 GYFHDATRVYLI---LEYAPLGVTVRELOKLSFDEQRTATYITELANALSYCHSKRVIH 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 --RKKEGFVYGSNPHK 226
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 RDIKPENLLGSGNELK 263
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 22
H64625
Type I restriction enzyme S protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: H64625
R;Tomb, J.F.; White, O.; Kervilave, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64625
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-298 <TOM>
A;Cross-references: UNIPROT:O25519; GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD0789

Query Match 6.7%; Score 116.5; DB 2; Length 298;
Best Local Similarity 23.9%; Pred. No. 2.5;
Matches 59; Conservative 45; Mismatches 86; Indels 57; Gaps 12;

QY 79 EVTPPV-----QSQKIDGSPKIGSVKLNKAQT-----LELSRFTLV-----120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 32 QITIPPLPIQBEIVKILDAFTL--NTELTALKARKQYQYQNNLLDFNDINQHKD 90
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 -KLGTTPK-----FDKVSQKGIIEEDFLVNLSDINAEQLSGDFLIRRS 164
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 91 AKITYPKRLKTLTLHTLAPKGVFRKLK--EVCEINKKTLKISEVSEVKNKGWYVINS 148
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 DDLFYGYHYHTN--GKNLVDA--DKFSQYFVYDEKRVNDNISDKLTATYRKKEGFVYGS 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 GRDLGYGYHDFNNDGENITIASRGEVAGFINYFNK-----FFAGGLCYPKYKVD-----T 199
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 NPHTKFAARISKLDVSEIKFENGQAQSKDKENGAIEFTIKGDTKQLEIPTPSNRI 281
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 200 NELLTKFLYFLYKTEIQL--MENLVFRGSPALNKADIETLTI-----PIPLPIQBE 251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 282 IIAILDQ 288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 252 IVKILDQ 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 23
E81003
Transferin-binding protein-related protein NMB2132 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
```

```
C;Accession: E81003
R;Hickel, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
R;Key, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: E81003
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 <TET>
A;Cross-references: UNIPROT:Q9JOW0; GB:AE002561; GB:AE002098; NID:g7227384; PIDN:AAF4244
A;Experimental source: serogroup B, strain MCS8
C;Genetics:
A;Gene: NMB2132

Query Match 6.7%; Score 116; DB 2; Length 488;
Best Local Similarity 25.6%; Pred. No. 5.2;
Matches 57; Conservative 18; Mismatches 82; Indels 66; Gaps 11;

QY 4 SSGSGSSSTPHH-PKPVLPVPTQNNLQANVPQQAQNAQAQNA-----PQA 54
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 105 NAAGTDSSTPHHTPPNVLGNMEN-----QATDAGESSQANQPMANAAQMGQDDPSA 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 --QNAQVANAQAQNAQVANAQAQVTPVPQSQKIDGS-----FDXIGSVKLNKE 107
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 GQQAQNT-----AAQANQAGNNQAAGSSDIPASNPAPANGSGNFGVLDLNGVLIDGP 216
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 108 AQTLELSRFTLVDLKGTTPKPKVSGKKIIEBKDFLVNLSDINAEQLSGDFLIRSDDL 167
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 217 SQNITL-----THCKGDCSGNNFLDEE-----VQLKSEFEKLSDADK 254
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 168 FVGYHYDHTNGKVLDAADKF-----SQYFVYVYDEK 197
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 255 ISNYKKD--GKN-----DKFVLVADSVQMGKINGQIIFYPK 290
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 24
F90603
Vipe-like (mycoplasma hyorhinis) lipoprotein [imported] - Mycoplasma pulmonis (strain UAI
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: F90603
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: F90603
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-682 <KUR>
A;Cross-references: UNIPROT:Q98PI8; GB:AL445566; PID:g14090149; PIDN:CAC13907.1; GSPDB:G
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_7340
A;Genetic code: SGC3

Query Match 6.7%; Score 115.5; DB 2; Length 682;
Best Local Similarity 19.1%; Pred. No. 8.5;
Matches 73; Conservative 53; Mismatches 126; Indels 131; Gaps 17;

QY 10 SSTNHPK-----FVLVPTQNNLQAO-----NVFQAQNASQAQ--NAPQAQNAQAQNA 57
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 SQTNNPNVVEEQKSDSPKAPDTQDSGKQEBELKSPSSPDAGSQQSPESQNPSTPNSDK 142
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 PQVANAQA-----QNAQOVEN-----APQAEVTPVPQSQKIDGSFD 97
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 DQKPEPQAPKSKDENQMLGESQTPDTPNVEDTQEPAPQSP--NPEENNSEENWDSND 201
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 98 KIGSVKLNKAQTLBLSRFTLVDLKGTTPKPKDK-----VSGKKIIEEDFLVNLSDINA 152
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 K-----EKESKPKWKEKSENAPVELINIISDGENLWLNFKDAFS 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```





N;Alternate names: ORF-3  
C;Species: Pneumocystis carinii  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: JC2301  
R;Wada, M.; Nakamura, Y.  
DNA Res. 1, 163-168, 1994  
A;Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis  
A;Reference number: JC2299; MUID:96051989; PMID:8535973  
A;Accession: JC2301  
A;Molecule type: DNA  
A;Residues: 1-430 <WAD>  
A;Cross-references: UNIPROT:Q01823; GB:D31909; GB:D17441; NID:9559718; PIDN:BAA06706.1;

Query Match 6.5%; Score 112.5; DB 2; Length 430;  
Best Local Similarity 30.0%; Pred. No. 7.3;  
Matches 27; Conservative 13; Mismatches 37; Indels 13; Gaps 2;

QY 6 SGSSSTNHPKPVLPKTNQLQAQNVQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 65  
Db 249 STSSSPPP 300

QY 66 AQNAQVNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 90  
Db 301 PEPPE 330

RESULT 29  
T26449  
hypothetical protein Y113G7B.23 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T26449  
R;Lennard, N.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z20215  
A;Accession: T26449  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-366 <WIL>  
A;Cross-references: UNIPROT:Q902W6; EMBL:AL110477; NID:e1542121; PIDN:CAB54337.1; CESP:Y  
A;Experimental source: clone Y113G7B  
C;Genetics:  
A;Gene: CESP:Y113G7B.23  
A;Introns: 318/1

Query Match 6.4%; Score 111.5; DB 2; Length 366;  
Best Local Similarity 28.3%; Pred. No. 6.9;  
Matches 28; Conservative 12; Mismatches 34; Indels 25; Gaps 2;

QY 16 PKPVLVPTKTNQLQAQNVQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 75  
Db 139 PQP--TPQVLSAQEAAPFEMDTSEATAAPPTPQAPQAPVQAAPVQAAPQA 196

QY 76 P-----QAETPPVPQSQK 91  
Db 197 PQAQYGYGGGPPQQAQYVPQGGQYSPYPPQOQ 235

RESULT 30  
A90575  
conserved hypothetical protein MYPV\_5050 [imported] - Mycoplasma pulmonis (strain UAB CT  
C;Species: Mycoplasma pulmonis  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: A90575  
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Sanson, D.; Gallison, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm  
A;Reference number: A99512; MUID:21267165; PMID:11353084  
A;Accession: A90575  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-833 <KUR>  
A;Cross-references: UNIPROT:Q98Q63; GB:AL445566; PID:G14089919; PIDN:CAC13678.1; GSPDB:G

N;Experimental source: strain UAB CTIP  
C;Genetics:  
A;Gene: MYPV 5050  
A;Genetic code: SGC3

Query Match 6.4%; Score 111.5; DB 2; Length 833;  
Best Local Similarity 20.3%; Pred. No. 20;  
Matches 92; Conservative 60; Mismatches 141; Indels 161; Gaps 25;

QY 20 LVPKTONNLAQ-----NVQAQNASQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 70  
Db 56 LIPK--NNLDYRQAPNTDNLEIQEPLPEPKPEEPQPLPEPEPEPEPEPEPKPEPEP 113

QY 71 QVENAPQAEVTPVPQPSQKI-----DGSF-DKI-----GS 101  
Db 114 KPAPLPKEIPKIPKPPQKPLPPQKVEBPCKTTPPIRQSKPSDEAKEGQIVDXIVKFG 173

QY 102 VKLN--KEATLSELSRFTLVKLG-----TPPKFDK-----VSGKK 135  
Db 174 VDIKVKRTPTRKVSQKIDDKIANRPNRYNDIADHVISAEVTPFIEKRNQRLGKLG 233

QY 136 --IIEKDFL--VLNL--SDIN--AEQLSG--DFLIR----- 162  
Db 234 QNFLANQNFLLNNAKESDVYKIADHLAGNPTFETRVIAKFKQLIDDPNWNPNLHNR 293

QY 163 --RSDDLFGYHYDHTNGKLVDAADKFSQYFVYDE-----KRVNDNIS--DKLTA 209  
Db 294 DYRGD-----DTPPDNL--ELQKFLKNGYTLDDVKKLABIRKKRIQEVVDDYDPAK 343

QY 210 TYRKKEGFPVGSN-----PHTKEFAARISKLGDEVI--KFENGQAQ-----GSIKDEK 256  
Db 344 DPKKKIKCYGPNCFEGKKGHVLEYIYRTINMIDTNLTFLKDSNTEGDIRKGYVIDEEN 403

QY 257 GNAEFTIKGDTKOLEITPTESNRILIALDNOK-----SYTQGM 297  
Db 404 DNVFI--NSKGEINSYKAPLINGTKILYKXDNTERAFGYSSWNRFGQIGESY--FGW 461

QY 298 EKAIMET-----KPIDSKAGNSDKYLIGEAQSD 326  
Db 462 TKTDITTSPEYKKYKNSKRDGINISKLTRDVKSD 495

RESULT 31  
B40713  
cylicin I - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 09-Jul-2004  
C;Accession: B40713; S35920  
R;Hess, H.; Heid, H.; Franke, W.W.  
J. Cell Biol. 122, 1043-1052, 1993  
A;Title: Molecular characterization of mammalian cylicin, a basic protein of the sperm h  
A;Reference number: A40713; MUID:93359502; PMID:8354692  
A;Accession: B40713  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-598 <HES>  
A;Cross-references: UNIPROT:P35663; GB:Z22780; NID:G396104; PIDN:CAA80457.1; PID:G396105  
C;Keywords: cytoskeleton

Query Match 6.4%; Score 111; DB 2; Length 598;  
Best Local Similarity 21.6%; Pred. No. 14;  
Matches 79; Conservative 51; Mismatches 142; Indels 94; Gaps 16;

QY 7 GGSSSTPNHPKPVLPKTNQLQAQNV---QAQNASQAQNAQNAQNAQNAQNAQNAQNA 63  
Db 82 GGSYATNPESKQIVBEKTKRQNEADKTLKSSHENEQSKSKSSSETNPESQNSKTIV--- 138

QY 64 QAQNAQVNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 123  
Db 139 --SKNCSQKDKX-----DSKNSKKTNTBFLHTK----- 164

QY 124 TPKPKD---KVSQKKIIEKDFLVNLSDINAEQLSGDFLIRRDLLFYGY-----YH 173



```

150 SPCKFTTYKVHNSIEVNRFSSTPTKLLTNPHKVAIAINDEHYVWSNESIEENIEVAHLEN 209
75 APAQEVTPVPQOSQKIDGSPKIGSVKLNKEAQTLELSRFT-----LVDKLGTPEPKFDK 130
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
210 VFRSSPTPDEQBE-----YMKLGIRLSSSSYGGSSIKSENSLPKVLDELQSQNEEIK 262
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
131 VSGKKIIEKDFVLNLSDNAEQSGDFLIRRSDDLFGYYHDTN--GKNLVDAADKFS 198
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
263 ALFQK-LEEKDDRIQHELENS--MNDAKLQRIEDLQKEFHNERKAASKRLNIVQDRFR 318
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
189 QYFVVVDEKRVND-----NISDKLTATVRKKEGFVGSNPHTKEFAAR---ISKLGDEVEIK 241
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
319 KEIKKIREEXTIDPQNKAS-----KKEKNVTSAKTKCKAFSQRNLSLYRKKQKQ 371
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
242 FENQAQGS--IDKXGDNAAEIFTKGDTKOLEITPTESNRILAILDONQKSYTPG--M 297
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
372 ILNQENDXFLKDNESNNISIVKLRSEVELKSNLQSQ-----DENKXLHDNGSFY 424
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
298 EKAIMET-----KFI--DSKAGNSDQKYLIGEAK 324
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
425 EKRLNDVYSYMONLSLPEKDLGKFLIEEMKCGHSPMFQNGFAK 468
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 36
S64146
probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G2842
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64146; P:7139
R;Escribano, V.; Erasó, P.; Portillo, F.; Mazon, M.J.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64144
A;Accession: S64146
A;Molecule type: DNA
A;Residues: 1-1264 <ES>
A;Cross-references: UNIPROT:P53125; EMBL:Z72655; NID:gl322701; PID:e243361; PID:gl322702;
A;Experimental source: strain S288C
R;Escribano, V.; Erasó, P.; Portillo, F.; Mazon, M.J.
Yeast 12, 887-892, 1996
A;Title: Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces cerevisiae chromosome
A;Reference number: S71733; MUID:96437978; PMID:8840506
A;Accession: S71739
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1264 <ES>
A;Cross-references: EMBL:X92670
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Gene: SGB:ITC1
A;Cross-references: SGD:S0003101
A;Map position: 7L
C;Keywords: transmembrane protein
F;549-565/Domain: transmembrane #status predicted <TMM>

Query Match 6.3%; Score 110; DB 2; Length 1264;
Best Local Similarity 19.5%; Pred. No. 42;
Matches 86; Conservative 51; Mismatches 137; Indels 168; Gaps 18;

QY 4 SGGSGSSSTPNHP-----KPVLYPKTQNNLQAQNVPOAQN-ASQAQNAPOAQNAP 52
DB 298 SKSSGKNTSNDASNKKETKKRKPTEVNDSENNSEEDKKGQNVTSETHSKRKKEAN 357
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
53 QAQNAPOVENAPOAQNAPOVENAQA-----EVTTPVPOQ----- 88
DB 358 EEPNTENVESYPTPANA-----EPOAVTITSIMDLALFVQHPNFIFFNLTYNEKLECI 412
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
89 --SOKIDGSPDKGVSVK----LNKEAQTLELSRFTLVDKLGTPEPKF----- 128
DB 413 SLGSKLSPRPSDFGKLQAQVFLNTPFSKICLSHFSL-DQFITSKCTDPYELKGSEVL 471
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
129 ----DKVSGKKIIEBKDFVLNLSDNAEQS-----GDFLIRR-SDDIFYGY 171
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 17, 2004, 15:57:34 ; Search time 175.595 Seconds  
(without alignments)  
686.754 Million cell updates/sec

Title: US-10-696-544-2  
Perfect score: 1734  
Sequence: 1 CGSGSGSGSSPTNHPKPV.....YLIGAKSDNQWQIMVSEKK 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep:  
2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep:  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep:  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep:  
5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep:  
6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep:  
7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep:  
8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:  
9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep:  
10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep:  
11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep:  
12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep:  
13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep:  
14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep:  
15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep:  
16: /cgn2\_6/prodata/2/pubpaa/US10D\_PUBCOMB.pep:  
17: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep:  
18: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep:  
19: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep:  
20: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1734	100.0	337	16	US-10-696-544-2
2	221.5	12.8	335	15	US-10-406-686A-41
3	219	12.6	43	16	US-10-696-544-12
4	186.5	10.8	1164	9	US-09-797-385-10
5	178.5	10.3	1104	9	US-09-797-385-4
6	177	10.2	1164	9	US-09-797-385-2
7	173	10.0	1128	9	US-09-797-385-6
8	168	9.7	1098	9	US-09-797-385-8
9	141	8.1	3164	17	US-10-669-161-72
10	140.5	8.1	730	9	US-09-748-875-68
11	140.5	8.1	730	10	US-09-298-523B-68
12	137.5	7.9	756	17	US-10-425-115-288440
13	135	7.8	94	16	US-10-767-701-56462

14	132.5	7.6	447	14	US-10-156-761-9880	Sequence 9880, Ap
15	129.5	7.5	238	17	US-10-739-930-10816	Sequence 10816, A
16	129	7.4	409	16	US-10-771-931-33	Sequence 33, Appl
17	127	7.4	448	15	US-10-244-596-14	Sequence 14, Appl
18	125.5	7.2	1036	15	US-10-382-122A-64159	Sequence 64159, A
19	124.5	7.2	784	17	US-10-425-115-301016	Sequence 301016, A
20	124	7.2	631	14	US-10-043-344-115	Sequence 115, App
21	122	7.0	599	15	US-10-382-122A-63567	Sequence 63567, A
22	121.5	7.0	1013	17	US-10-807-746-14	Sequence 14, Appl
23	121	7.0	315	17	US-10-425-115-281769	Sequence 281769, A
24	120.5	6.9	287	17	US-10-758-846-20	Sequence 20, Appl
25	120.5	6.9	306	15	US-10-112-944-413	Sequence 413, App
26	120.5	6.9	306	17	US-10-758-846-19	Sequence 19, Appl
27	120	6.9	430	16	US-10-771-931-54	Sequence 54, Appl
28	118	6.8	334	9	US-09-789-054A-4	Sequence 4, Appli
29	118	6.8	334	16	US-10-628-969-4	Sequence 4, Appli
30	117.5	6.8	456	16	US-10-771-931-13	Sequence 13, Appl
31	117.5	6.8	646	17	US-10-425-115-230961	Sequence 230961, A
32	117.5	6.8	806	16	US-10-771-931-9	Sequence 9, Appli
33	117.5	6.8	1009	16	US-10-771-931-7	Sequence 7, Appli
34	117.5	6.8	1046	16	US-10-771-931-1	Sequence 1, Appli
35	117	6.7	297	17	US-10-425-115-281772	Sequence 281772, A
36	117	6.7	2478	9	US-09-815-242-5816	Sequence 5816, Ap
37	117	6.7	2478	9	US-09-815-242-12967	Sequence 12967, A
38	116.5	6.7	298	10	US-09-882-227-138	Sequence 138, App
39	116.5	6.7	459	17	US-10-702-305A-18	Sequence 18, Appl
40	116.5	6.7	704	16	US-10-437-963-1855221	Sequence 1855221, A
41	116.5	6.7	2497	14	US-10-161-051-189	Sequence 189, App
42	116	6.7	464	15	US-10-220-480-2	Sequence 2, Appli
43	116	6.7	488	16	US-10-220-481-84	Sequence 84, Appl
44	116	6.7	488	16	US-10-220-481-619	Sequence 619, App
45	115.5	6.7	340	9	US-09-789-054A-6	Sequence 6, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-696-544-2  
; Sequence 2, Application US/10696544  
; Publication No. US20040156865A1  
; GENERAL INFORMATION:  
; APPLICANT: Confer, Anthony W  
; APPLICANT: Ayalew, Sahu  
; APPLICANT: Murphy, George  
; APPLICANT: Pandher, Karamjeet  
; TITLE OF INVENTION: M. Haemolytica Outer Membrane Protein plpE as a Vaccine or  
; TITLE OF INVENTION: Vaccine Component Against Shipping Fever  
; FILE REFERENCE: 03300-57188/02-744  
; CURRENT APPLICATION NUMBER: US/10/696,544  
; CURRENT FILING DATE: 2003-10-29  
; PRIOR APPLICATION NUMBER: US 60/422,305  
; PRIOR FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Mannheimia haemolytica  
; PUBLICATION INFORMATION:  
; AUTHORS: Pandher et al.  
; TITLE: Genetic and Immunologic Analyses of PlpE, a Lipoprotein Important  
; TITLE: In Complement-Mediated Killing of Pasteurella Haemolytica  
; TITLE: Serotype 1  
; JOURNAL: Infection and Immunity  
; VOLUME: 66  
; ISSUE: 12  
; PAGES: 5613-5619  
; DATE: 1998-12  
; US-10-696-544-2

Query Match 100.0%; Score 1734; DB 16; Length 337;  
Best Local Similarity 100.0%; Pred. No. 2.2e-123;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGSGSGSSSTPNHPKVLVPTKQNNLQAOVFPQAOVQASQAQNAPOAQAQNAPOV 60  
Db 1 CGSGSGSSSTPNHPKVLVPTKQNNLQAOVFPQAOVQASQAQNAPOAQAQNAPOV 60

QY 61 ENAPOAQAPOVNAPOAQAQVTPVPOQOSQKIDGFKIGSVKLNKEAQTLESLRFLVD 120  
Db 61 ENAPOAQAPOVNAPOAQAQVTPVPOQOSQKIDGFKIGSVKLNKEAQTLESLRFLVD 120

QY 121 KLGTTPKPKDKVSGKKIIEBKDFVLNLSDNAEQLSGDFLIRSDDLFYGYHDTNGKNL 180  
Db 121 KLGTTPKPKDKVSGKKIIEBKDFVLNLSDNAEQLSGDFLIRSDDLFYGYHDTNGKNL 180

QY 181 VDAADKFSQYFVYDEKRVNDSKLTATYRKKEGFVYGNPHTKFAARISKLGDEVI 240  
Db 181 VDAADKFSQYFVYDEKRVNDSKLTATYRKKEGFVYGNPHTKFAARISKLGDEVI 240

QY 241 KPEQAQGSIKDEXDGNAEFTTKGDTKOLEITPTESNRHIIAILDQNKSYTPGMEKA 300  
Db 241 KPEQAQGSIKDEXDGNAEFTTKGDTKOLEITPTESNRHIIAILDQNKSYTPGMEKA 300

QY 301 IMETKFDISKAGNSDKYLIKEAKSDNQAINVSEK 337  
Db 301 IMETKFDISKAGNSDKYLIKEAKSDNQAINVSEK 337

RESULT 2  
US-10-406-686A-41  
; Sequence 41, Application US/1040686A  
; Publication No. US20040033586A1  
; GENERAL INFORMATION:  
; APPLICANT: CROCKE, HELEN RACHEL  
; APPLICANT: SHEA, JACQUELINE ELIZABETH  
; APPLICANT: FELDMAN, ROBERT GRAHAM  
; APPLICANT: COUTEBROZE, SYLVAIN GABRIEL  
; APPLICANT: LEGROS, FRANCOIS-XAVIER  
; TITLE OF INVENTION: ATTENUATED GRAM NEGATIVE BACTERIA  
; FILE REFERENCE: 454313-3171.1  
; CURRENT APPLICATION NUMBER: US/10/406.686A  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: 60/370,282  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 335  
; TYPE: PRT  
; ORGANISM: Pasteurella multocida  
US-10-406-686A-41

Query Match 12.8%; Score 221.5; DB 15; Length 335;  
Best Local Similarity 22.8%; Pred. No. 1.4e-08;  
Matches 79; Conservative 58; Mismatches 160; Indels 49; Gaps 10;

QY 2 CGSGSGSSSTPNHPKVLVPTKQNNLQAOVFPQAOVQASQAQNAPOAQAQNAPOV 61  
Db 2 CGSGSAGNADRVBEK-----AQV-----QNSPSSAPIKNTNTATNDSLHD 67

QY 62 NAPAQAQNAPOVNAPOAQAQVTPVPOQOSQKIDGFS-----DKIGSVKLNKEAQTLESL 114  
Db 62 KLSMSSHDTSKENSQSSFKAPLEQKQPAQENLTWTGYHVSQVGNVNNVDKNDVTV- 126

QY 115 RFTLV---DKLGTPTKPKDKVSGKKIIEBKDFVLNLSDNAEQLSGDFLIRSDDLFYGY 171  
Db 127 -FTFVKYNSQNDPVPFDTKTQS-----KTSLVGKNENKEDYNTLTKDALF--- 175

QY 172 YHDTNGKNLVDADKFSQYFVYDEKRVNDSKLTATYRKKEGFVYGNPHTKFAAR 231  
Db 176 YGSGVQPSADYKKVKYNYIYAKPDALNNENLALATATYQEDGYFVSLSDVNRVGE 235

QY 232 -ISKLGDEVIKPENGQAQGSIKDEXDGNAEFTTKGDTKOLEITPTESNRHIIAILDQNK 290

Db 236 YIPQYGNVTLTFRNGKIYGEIYRYNRRDDLFLQSLSEGQNLITPHK-----DNPH 286

QY 291 KYTPTQMEKAINMETKFDISKAGNSDKYLIKEAKSDNQAINVSEK 336  
Db 287 KLSPTGPDNNAMELAFIN--AEKTDKKYVGVGKAEKYYGLLFAEK 330

RESULT 3  
US-10-696-544-12  
; Sequence 12, Application US/10696544  
; Publication No. US20040156865A1  
; GENERAL INFORMATION:  
; APPLICANT: Confer, Anthony W  
; APPLICANT: Aralew, Sahlu  
; APPLICANT: Murphy, George  
; APPLICANT: Pandher, Karamjeet  
; TITLE OF INVENTION: M. Haemolytica Outer Membrane Protein PlpB as a Vaccine or  
; FILE REFERENCE: 03300-57188/02-744  
; CURRENT APPLICATION NUMBER: US/10/696.544  
; CURRENT FILING DATE: 2003-10-29  
; PRIOR APPLICATION NUMBER: US 60/422,305  
; PRIOR FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 12  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Mannheimia haemolytica  
US-10-696-544-12

Query Match 12.6%; Score 219; DB 16; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.4e-09;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 QNASQAQNAPOAQAQNAPOVNAPOAQAQNAPOVNAPOAQAQNAPOVNAPOAE 79  
Db 1 QNASQAQNAPOAQAQNAPOVNAPOAQAQNAPOVNAPOAQAQNAPOVNAPOAE 43

RESULT 4  
US-09-797-385-10  
; Sequence 10, Application US/09797385  
; Publication No. US20020058042A1  
; GENERAL INFORMATION:  
; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Blake, Milan S.  
; TITLE OF INVENTION: Non-IgA Fc Binding Forms of the Group B  
; Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/797,385  
; FILING DATE: 01-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/923,992  
; FILING DATE: 05-SEP-1997  
; APPLICATION NUMBER: US 60/024,707  
; FILING DATE: (vid)  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.







```

; SEQ ID NO 72
; LENGTH: 3164
; TYPE: PRT
; ORGANISM: Herpes Virus
US-10-669-161-72

Query Match      8.1%; Score 141; DB 17; Length 3164;
Best Local Similarity 36.9%; Pred. No. 0.36;
Matches 41; Conservative 5; Mismatches 18; Gaps 3;

QY 2 GGSGGGS-SSTNHKPKVLVPKT-----QNNLQANVPQANASQAQN 44
DB 2872 GGAVPGGVSRRTTRQPVATETTSARPRGHILTVSRLSAPOFQPOQPOFQPOQPO 2931
QY 45 APOAQNAPOAQNAPOVENAPOAQNAPOVENAPOAEVTP-PVPOQSQKIDG 94
DB 2932 QPQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQPOQNG 2982

RESULT 10
US-09-748-875-68
; Sequence 68, Application US/09748875
; Publication No. US20010016200A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/748,875
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: 09/298,523
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 68
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-748-875-68

Query Match      8.1%; Score 140.5; DB 9; Length 730;
Best Local Similarity 35.8%; Pred. No. 0.056;
Matches 29; Conservative 16; Mismatches 35; Indels 1; Gaps 1;

QY 13 PNHPKPKVLVPTQNNLQANVPQANASQAQNAPOAQNAPOAQNAPOVENAPOAQNAPOV 72
DB 594 PEAPKSPKVPKVPKVPKAPDTPQVPEAPKSPKVPKVPKAPDTPQVPEAPKSPKVPK 653
QY 73 ENAPOAEVTPVPPO-POSQKI 92
DB 654 PEAPKAPDTPQVPEAPKSPKVP 674

RESULT 11
US-09-298-523B-68
; Sequence 68, Application US/09298523B
; Publication No. US20030059438A1
; GENERAL INFORMATION:
; APPLICANT: BRILES et al.
; TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEIN C (PSPC), EPITOPIC REGIONS
; TITLE OF INVENTION: AND STRAINS THEREOF AND USES THEREFOR
; FILE REFERENCE: 454312-3140
; CURRENT APPLICATION NUMBER: US/09/298,523B
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 68
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-298-523B-68

Query Match      8.1%; Score 140.5; DB 10; Length 730;

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Best Local Similarity 35.8%; Pred. No. 0.056;
Matches 29; Conservative 16; Mismatches 35; Indels 1; Gaps 1;

QY 13 PNHKPVLPVPTONNLOAQNVPOAQNASQAQNAPOAQNAPOAQNAPOAQNAPOAQNAPOV 72
Db 584 PEAPKSPVVKVPAPKAPDTPQVPEAPKSPVVKVSDTPKAPDTPQVPEAPKSPVVKV 653

QY 73 ENAPOAEVTPPVQ-POSQKI 92
Db 654 PEAPKAPDTPQVPEAPKSPV 674

RESULT 12
US-10-425-115-288440
; Sequence 288440, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 288440
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_26148C.1.pap
US-10-425-115-288440

Query Match 7.9%; Score 137.5; DB 17; Length 756;
Best Local Similarity 23.4%; Pred. No. 0.099;
Matches 86; Conservative 40; Mismatches 130; Indels 111; Gaps 18;

QY 16 PKPVLVPTONNLOAQNVPOAQNASQAQNAPOAQNAPOAQNAPOAQNAPOAQNAPOV 74
Db 429 PAP-----TKTBAAKTPAKAKTGAET--EATEAPQAPVEABAGPSAPIAAKPALEE 481

QY 75 APQAEVTPPVQPOS--QKIDGSPDKIGSVKINKE-----AQTLERSRFTLVDKLGT 124
Db 482 KSSGHIAPEPTAPALLETIDYIFRHASGKKLSEDEIAEARHYAQKLKYPKGLV----- 536

QY 125 PKPKDKVSGKKIIEKDFLV-----NLS-----DINAEQLSGDFLIRSDDLFVGY 172
Db 537 ---FNRS-----EYDFLYLVPNKLSVCREIGRIGFPKLEDDGLLILSKDDLADNLA 587

QY 173 HDTNGKLVDAAD-----KFSQVYVYDEKRVNDN--SDKLATATYRKKEGFVYVGSNP 223
Db 588 Y--NGMKLAEKENCALAEANREISEYQNYLEKRVEE-----LWQKERCPEKSLD 637

QY 224 HTKEFAARISKLG--DVEIKFENGQAQGS---IKDEKDGNAETFTIKDGTQKLEITPTES 278
Db 638 CVKIKKASFVKGAYSABENFIQDDEGVVWEINGEAEETFEILSDRGD----- 686

QY 279 NRITIAILDQKQSYTPGMKAKMETKFDISKAGNSQKYLIGBAKSDNW-----Q 329
Db 687 ---VCARSDDTK---DFSAEAILMGHGFY-----NDIWNQGREMAHE 723

QY 330 AIMVSEK 336
Db 724 IIMSEK 730

RESULT 13
US-10-767-701-56462
; Sequence 56462, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 56462
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30943377.pap
US-10-767-701-56462

Query Match 7.8%; Score 135; DB 16; Length 94;
Best Local Similarity 46.3%; Pred. No. 0.0095;
Matches 31; Conservative 7; Mismatches 23; Indels 6; Gaps 3;

QY 19 VLVPTQNNLOAQNVPOAQNASQAQNAPOAQNAPOAQNAPOAQNAPOAQNAPOV 78
Db 7 IVAPEQQENVQ----PQSQQ-PQTQNPQNAQNPQSQQQPQVQ--PQVQQQFPVQQQPV 60

QY 79 EVTPPV 85
Db 61 SSTTNEP 67

RESULT 14
US-10-156-761-9880
; Sequence 9880, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9880
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9880

Query Match 7.6%; Score 132.5; DB 14; Length 447;
Best Local Similarity 28.6%; Pred. No. 0.12;
Matches 34; Conservative 9; Mismatches 41; Indels 35; Gaps 1;

QY 2 GSGSGGSGSSSTPNHPKP-----VLPVKTQN 26
Db 15 GGGPGGSGSSTFGTDPSSASASASTPSTSGTSSPSGASSPSGTSTSTTS 74

QY 27 NLQAVFQAVQASQAQNAPOAQNAPOAQNAPOAQNAPOAQNAPOAQNAPOV 85
Db 75 STSAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAPDAP 133

RESULT 15
US-10-930-930-10816
; Sequence 10816, Application US/10739930
```

Publication No. US20040216190A1  
GENERAL INFORMATION: David K.  
APPLICANT: Kovalic, David K.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-21(53377)B  
CURRENT APPLICATION NUMBER: US/10/739,930  
CURRENT FILING DATE: 2003-12-18  
NUMBER OF SEQ ID NOS: 11088  
SEQ ID NO 10816  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Triticum aestivum  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(238)  
OTHER INFORMATION: unsure at all xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: TRIA3-23APR03-C730\_1224.P  
US-10-739-930-10816

Query Match 7.5%; Score 129.5; DB 17; Length 238;  
Best Local Similarity 45.8%; Pred. No. 0.086;  
Matches 33; Conservative 2; Mismatches 34; Indels 3; Gaps 2;

QY 18 PVLVPTQNNLQAVNQVPOAQNASCAQNAPOAQNAPQVNAPOAQNAPQVNAPO 77  
Db 21 PVQPTTEVAPAGNPPAPNAPPAGNPPAPVPPAGNPPAPAPPTTP--PQAP 78

QY 78 AEVTPPVPOQS 89  
Db 79 APATPP-PAPQA 89

RESULT 16  
US-10-771-931-33  
Sequence 33, Application US/10771931  
Publication No. US20040151737A1  
GENERAL INFORMATION:  
APPLICANT: Courtney, Harry  
TITLE OF INVENTION: Streptococcal Serum Opacity Factors And Fibronectin-Binding Prote  
FILE OF INVENTION: Peptides Thereof For The Treatment And Detection Of Streptococci  
FILE REFERENCE: 13314.1001U  
CURRENT APPLICATION NUMBER: US/10/771,931  
CURRENT FILING DATE: 2004-02-04  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 409  
TYPE: PRT  
ORGANISM: Streptococcus pyogenes  
US-10-771-931-33

Query Match 7.4%; Score 129; DB 16; Length 409;  
Best Local Similarity 20.8%; Pred. No. 0.19;  
Matches 73; Conservative 57; Mismatches 123; Indels 98; Gaps 15;

QY 4 SGSGSGSSTPHKPKVLPVPTQNNLQAVNQVPOAQNASCAQNAPOAQNAPQVNAPOA 63  
Db 14 SGAGSESSDAS-----VVPSEGSQSGTTTP-----ASKQPOAQTAPATASSTSS 61

QY 64 PQQNAPO-----VENAPO-----EVTTPVPOQSQKIDG-SFDKIGSVKLN----- 105  
Db 62 SSDGKAPQAATISTSTPAAGTSNSNQVTGTETAEPTQMDVRYTVDKENS-KLNTKGD 120

QY 106 -----KEAQTLELSRFTLVKLGTPPKFKDKYSGKKIIEEKDFLVL 145  
Db 121 KPNKRSSVDKDKLNRDQKQORDIVDTVTXKTNEDGTTDVTVTVPKQIDGAD--VM 178

QY 146 NLGDINAEQSGDFILRRSDDLFGYYHYHDNGKNLVDAADKFSQYFVYDKEKVN--DNI 203  
Db 179 ALLDVSKMKSEDDF-----NNAKDKIKKLVTTLTSTKSGANGQQL 217

Publication No. US20040216190A1  
GENERAL INFORMATION: David K.  
APPLICANT: Kovalic, David K.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-21(53377)B  
CURRENT APPLICATION NUMBER: US/10/739,930  
CURRENT FILING DATE: 2003-12-18  
NUMBER OF SEQ ID NOS: 11088  
SEQ ID NO 10816  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Triticum aestivum  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(238)  
OTHER INFORMATION: unsure at all xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: TRIA3-23APR03-C730\_1224.P  
US-10-739-930-10816

Query Match 7.5%; Score 129.5; DB 17; Length 238;  
Best Local Similarity 45.8%; Pred. No. 0.086;  
Matches 33; Conservative 2; Mismatches 34; Indels 3; Gaps 2;

QY 18 PVLVPTQNNLQAVNQVPOAQNASCAQNAPOAQNAPQVNAPOAQNAPQVNAPO 77  
Db 21 PVQPTTEVAPAGNPPAPNAPPAGNPPAPVPPAGNPPAPAPPTTP--PQAP 78

QY 78 AEVTPPVPOQS 89  
Db 79 APATPP-PAPQA 89

RESULT 16  
US-10-771-931-33  
Sequence 33, Application US/10771931  
Publication No. US20040151737A1  
GENERAL INFORMATION:  
APPLICANT: Courtney, Harry  
TITLE OF INVENTION: Streptococcal Serum Opacity Factors And Fibronectin-Binding Prote  
FILE OF INVENTION: Peptides Thereof For The Treatment And Detection Of Streptococci  
FILE REFERENCE: 13314.1001U  
CURRENT APPLICATION NUMBER: US/10/771,931  
CURRENT FILING DATE: 2004-02-04  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 409  
TYPE: PRT  
ORGANISM: Streptococcus pyogenes  
US-10-771-931-33

Query Match 7.4%; Score 129; DB 16; Length 409;  
Best Local Similarity 20.8%; Pred. No. 0.19;  
Matches 73; Conservative 57; Mismatches 123; Indels 98; Gaps 15;

QY 4 SGSGSGSSTPHKPKVLPVPTQNNLQAVNQVPOAQNASCAQNAPOAQNAPQVNAPOA 63  
Db 14 SGAGSESSDAS-----VVPSEGSQSGTTTP-----ASKQPOAQTAPATASSTSS 61

QY 64 PQQNAPO-----VENAPO-----EVTTPVPOQSQKIDG-SFDKIGSVKLN----- 105  
Db 62 SSDGKAPQAATISTSTPAAGTSNSNQVTGTETAEPTQMDVRYTVDKENS-KLNTKGD 120

QY 106 -----KEAQTLELSRFTLVKLGTPPKFKDKYSGKKIIEEKDFLVL 145  
Db 121 KPNKRSSVDKDKLNRDQKQORDIVDTVTXKTNEDGTTDVTVTVPKQIDGAD--VM 178

QY 146 NLGDINAEQSGDFILRRSDDLFGYYHYHDNGKNLVDAADKFSQYFVYDKEKVN--DNI 203  
Db 179 ALLDVSKMKSEDDF-----NNAKDKIKKLVTTLTSTKSGANGQQL 217

QY 204 SD-----KLTATYRKKEGFFVYGSNPHTKEFAARISKLGDVLEIKPENG----QAQSIKDEK 255  
Db 218 NNRNVTLMFTYRKISPIDLSGKTSSEVEEELNKIWD-KVYKDWGVDLQGAHKAH 276

QY 256 DGMAEITIKGDTKQLBITTESNRILAILDQNKQSYTPCMEKAIMETXF 306  
Db 277 D-----IFKKEKSKK-----RQHIVLFQSGESTFSVELHNSVKEDKY 314

RESULT 17  
US-10-244-596-14  
Sequence 14, Application US/10244596  
Publication No. US20040053238A1  
GENERAL INFORMATION:  
APPLICANT: Hsueh, Ruey-Shyang  
APPLICANT: Huang, Ya-Hui  
TITLE OF INVENTION: No. US20040053238A1 recombinant xylanases derived from anaerobic  
FILE OF INVENTION: relevant sequences, expression vectors and hosts  
FILE REFERENCE: P22617  
CURRENT APPLICATION NUMBER: US/10/244,596  
CURRENT FILING DATE: 2002-09-17  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14  
LENGTH: 448  
TYPE: PRT  
ORGANISM: Neocallimastix patriciarum  
US-10-244-596-14

Query Match 7.3%; Score 127; DB 15; Length 448;  
Best Local Similarity 36.8%; Pred. No. 0.31;  
Matches 35; Conservative 10; Mismatches 44; Indels 6; Gaps 4;

QY 2 GSXSGSGSSTPHKPKVLPVPTQNNLQAVNQVPOAQNASCAQNAPOAQNAPQVNAPOVE 61  
Db 240 GGAPAGAGAGNDQPOG---PQGOQPPGQPPGQPPGQPPGQPPGQPPGQPPGQPPGQ 295

QY 62 NAOQAQNAPOVENAQAQVTPFPVQ-PQSXKIDGS 95  
Db 296 QPPQGOQPPGQNDQGOQGO-QPPQGOQPPGQNDGPGGS 329

RESULT 18  
US-10-282-122A-64159  
Sequence 64159, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09









; ORGANISM: Homo sapiens  
US-10-112-944-413

Query Match 6.9%; Score 120.5; DB 15; Length 306;  
Best Local Similarity 25.7%; Pred. No. 0.58;  
Matches 56; Conservative 22; Mismatches 89; Indels 51; Gaps 9;

QY 2 GSGSGSSSTP--NHKPKVLVPTKQNNLOAQNVPOAQNASQAQNAPOAQNAPOAQNAPO 59  
DB 86 GIKDQSGSGSPGKHGPKGLAGPMGEKGLRGTPGQCKGNKGDVGTGPGEGPRGNIGPL 145  
QY 60 VENAPQAQNAPOVENAPQAQNAPOAETPPVPQ--POSQKI-----DGSFDKIG-SVKLNKEAQT 110  
DB 146 GPTGLPGMPGPIGPKGPKGEAGPTGPGQGVQGIKGMKGDGKEGKIGETLVLPKSAFT 205  
QY 111 L---ELSRFTLVKLGTPPKFDKV-----SGKKIIEEKD----- 141  
DB 206 VGLTVLSKFPSSDR---PIKFDKIHTVFRNVQVSLVKNVGLKILHTKDAYMSSDAQSG 262  
QY 142 --FLVLNLSD-----INAEQLSGDFLIIRSDDLFYGY 171  
DB 263 GIVLQLKLGDEVMQLVGTGGERFNGLFADEDDDTFTGTF 300

## RESULT 26

US-10-758-846-19

; Sequence 19, Application US/10758846

; Publication No. US20040248156A1

; GENERAL INFORMATION:

; APPLICANT: Hu, Tianhua

; APPLICANT: Tang, Y. Tom

; APPLICANT: Ghosh, Makabika

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wang, Zhiwei

; APPLICANT: Zhao, Qing

; APPLICANT: Xu, Chongjun

; APPLICANT: Mulero, Julio J.

; TITLE OF INVENTION: Methods and Materials Relating to Novel Clq Domain-containing

; FILE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-46CIP

; CURRENT APPLICATION NUMBER: US/10/758,846

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: PCT/US02/38526

; PRIOR FILING DATE: 2003-12-03

; PRIOR APPLICATION NUMBER: US 10/005,499

; PRIOR FILING DATE: 2001-12-03

; PRIOR APPLICATION NUMBER: US 10/296,115

; PRIOR FILING DATE: 2003-06-24

; PRIOR APPLICATION NUMBER: PCT/US00/35017

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 09/488,725

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 10/286,897

; PRIOR FILING DATE: 2002-11-01

; PRIOR APPLICATION NUMBER: US 10/258,898

; PRIOR FILING DATE: 2003-07-21

; PRIOR APPLICATION NUMBER: PCT/US00/34263

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/620,312

; PRIOR FILING DATE: 2000-07-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 125

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-758-846-19

## Query Match

Best Local Similarity 25.7%; Score 120.5; DB 17; Length 306;

; Sequence 19, Application US/10758846

; Publication No. US20040248156A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

## RESULT 28

US-09-789-054A-4

; Sequence 4, Application US/09789054A

; Publication No. US20020184659A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

Matches 56; Conservative 22; Mismatches 89; Indels 51; Gaps 9;  
QY 2 GSGSGSSSTP--NHKPKVLVPTKQNNLOAQNVPOAQNASQAQNAPOAQNAPOAQNAPO 59  
DB 86 GIKDQSGSGSPGKHGPKGLAGPMGEKGLRGTPGQCKGNKGDVGTGPGEGPRGNIGPL 145  
QY 60 VENAPQAQNAPOVENAPQAQNAPOAETPPVPQ--POSQKI-----DGSFDKIG-SVKLNKEAQT 110  
DB 146 GPTGLPGMPGPIGPKGPKGEAGPTGPGQGVQGIKGMKGDGKEGKIGETLVLPKSAFT 205  
QY 111 L---ELSRFTLVKLGTPPKFDKV-----SGKKIIEEKD----- 141  
DB 206 VGLTVLSKFPSSDR---PIKFDKIHTVFRNVQVSLVKNVGLKILHTKDAYMSSDAQSG 262  
QY 142 --FLVLNLSD-----INAEQLSGDFLIIRSDDLFYGY 171  
DB 263 GIVLQLKLGDEVMQLVGTGGERFNGLFADEDDDTFTGTF 300

## RESULT 27

US-10-771-931-54

; Sequence 54, Application US/10771931

; Publication No. US20040151737A1

; GENERAL INFORMATION:

; APPLICANT: Courtney, Harry

; TITLE OF INVENTION: Streptococcal Serum Opacity Factors And Fibronectin-Binding Protei

; FILE OF INVENTION: Peptides Thereof For The Treatment And Detection of Streptococcal

; FILE REFERENCE: 13314.1001U

; CURRENT APPLICATION NUMBER: US/10/771,931

; CURRENT FILING DATE: 2004-02-04

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 54

; LENGTH: 430

; TYPE: PRT

; ORGANISM: Streptococcus pyogenes

US-10-771-931-54

## Query Match

Best Local Similarity 6.9%; Score 120; DB 16; Length 430;

Matches 76; Conservative 46; Mismatches 152; Indels 52; Gaps 13;

QY 3 GSGSGSSSTENHPKPLVPK---TONNLOAQNVPOAQNASQAQNAPO--QAQNAPOAQNA 57  
DB 34 GTSGTAAGTGTGSDVSVSSESGSQAQASPOQAAPAAETTPKAQAQAAPVASAS 93  
QY 58 PQVENAPQAQNAPOVENAPQAQNAPOAETPPVPQ-----QPOSQKIDGSDFKIGSVKLNKEAQT 111  
DB 94 TTASSASSNVKTPKTESATISS--TPAVASSNGSNQASAEETPCQMDVQYKVNKKTTEL 152  
QY 112 ELSRFTLVKLGTPPKFDKV--SGKKIIEEKDFLVNLSDINAEQLSGDFLIIRSDDLFY 169  
DB 153 TV-----KDGTPKNGRTVNQNTKLIRNDRGQRDIFDKRE-----VKTNADGTI 198  
QY 170 GYVHTNGKNLVDAAD-----KFSQYFVYVYDEKRVNDNISDKLTA--TYRKKEGFVYGSNP 223  
DB 199 DVTVTVPKEIDEGADYMALLDVSKMTEEDFKNAKDKIKLVLTLTGDKREASFTNSV 258  
QY 224 HTKFFAARISKLDGVEIKFEN-----GQAGSGTIDKDKGNABEFTIKGDT-KLEIITPT 276  
DB 259 RLMTFYREISDPIDISGKTDDLDKLLKLEQAEKDECDMGVD---LQGAHKAAREVFN 315  
QY 277 ESN-----RIIIAILDQNKSYT 294  
DB 316 ENNSKKSKSGRQHIVLFSQGSTFS 341

## RESULT 28

US-09-789-054A-4

; Sequence 4, Application US/09789054A

; Publication No. US20020184659A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve



Best Local Similarity 19.9%; Pred. No. 2.6;  
Matches 77; Conservative

QY 4 SGGSGSSSTPNHP-----KPVLPKTKQNNLQA-----QNVFQAQNASQ 41  
Db 244 SGKVDASAAPSEPAKSKKLVLTTHRPHYETPTWVPEFGGETSSAATPKPEIPSTQKAE 303

QY 42 AQNAPQAQNAPOQNAPOVENAQAQNAPOVENAQAQNAQAEVTPP---VPOPSOKIDGDFK 98  
Db 304 PATLPKAPSAKLAE--PKTDKABEL-----RIGTKTLEVLSPSAEVTMPKAQK--GKIAK 355

QY 99 IGSVKLNKEAQTLELSRFTL---VDKLGTPPKFDKVS--GKKIIEKDFVLNLSDNA 152  
Db 356 ASKVPIETKTLE-AKATWSQASAEAGPEPAKEKPESEIGEKAAEE-----AISQILP 409

QY 153 EQLSGDFLRRDDLFGYHYDTHNGKLVDAADKFSQYF---VYDEKRVNDNISKLTA 209  
Db 410 EKAAPTPEAPSEDLGVIIIRH-ASGKRLSEENFEAKHYARELYKSGKALVFNQTD---464

QY 210 TYRKKEGFVYSGNPHTKFEPA-----ARISKLGDFVEI-----KPFENGAQGSIKD--253  
Db 465 ----EDDFLY-CLPDNKLVSCEMARSMGFPKLEAGLCAMTKDNLANSLAYNSLKGIL 519

QY 254 ----EKDGNAE-----IFTIKGDTKQLSEITTESNRHIIAILDQNKQSYTPGMEKAIM 302  
Db 520 SNALRAQNAADESCTIALLNATEVIRLNEATEKDKILLTLVDK-----I 566

QY 303 ETRFIDSKAGNSDKYLIGEAQSDN-W 328  
Db 567 KTSFANVGAYSSEDNFIRGDPGVNEW 593

RESULT 32  
US-10-771-931-9  
; Sequence 9, Application US/10771931  
; Publication No. US20040151737A1  
; GENERAL INFORMATION:  
; APPLICANT: Courtney, Harry  
; TITLE OF INVENTION: Streptococcal Serum Opacity Factors And Fibrinectin-Binding Prote  
; TITLE OF INVENTION: Peptides Thereof For The Treatment And Detection Of Streptococ  
; FILE REFERENCE: 131314.1001U  
; CURRENT APPLICATION NUMBER: US/10/771.931  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 806  
; TYPE: PRT  
; ORGANISM: Streptococcus pyogenes  
US-10-771-931-9

Query Match 6.8%; Score 117.5; DB 16; Length 806;  
Best Local Similarity 23.0%; Pred. No. 3.5;  
Matches 78; Conservative 47; Mismatches 131; Indels 83; Gaps 16;

QY 6 SGGSSSTPNHPKPVLPKTKQNNLQAQNVQA-----QNASQAQNAPOQNAPOQNAQ 58  
Db 38 NGGQSTP-----AVAEATPQQAQIAPVAAATSTSSAGSSSDGKAPQAVTSTSPSTP 91

QY 59 QVENAQAQNAPOQNAPOQNAQAEVTPPVPQSQKI---DGSFQKIGSVKLNKEAQT-----110  
Db 92 AAASSNGSQEASAEETPQMEVEKYIVDXENSKLNKDKGKTPKGS-SVNNKDKTLIR 150

QY 111 -----LELSRFTLVLDKLTGTPPKFDKVSQKIIIEKDFVLNLSDNAQISGDFLI 161  
Db 151 NRDKLRDIDVTRTVKTNEDGTTIDVTVTKQIDEGAD--VNALLDVSKQMSDDF--206

QY 162 RRSDDLFGYHYDTHNGKN---LYDAADKFSQYVVVYDEKRVNDNISDKLTATYRKKEGF 217  
Db 207 -----NNAQNKIKLVLTLSKASNSDNDHEKYNRSNVRMLMTYREI---250

QY 218 VYGSNP-----HTKEFAARISKLGD-----VEIKFENG-QAQSISKDEKQNAEIFTIK 266

```
Query Match      6.8%; Score 117.5; DB 16; Length 1046;
Best Local Similarity 23.0%; Pred. No. 5;
Matches 78; Conservative 47; Mismatches 131; Indels 83; Gaps 16;

QY 6 SGGSSSTNHKPVLPVKTQNNLQANVPQA-----QNASQANAPQANAPQANAP 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 NGGPSTP-----AVAEATPQQAQAPVAAATSTSSSSDGKAPQAVTSTSPSTP 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 59 QVENAPQANAPQVENAPQA-EVTPPVQPOSQKI---DGSFDDKIGSVKLNKEAQT--- 110
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 AAASNGSNQASAEETETQTEVEKYTVDKNSKLNKIDGKTPKTS-SVNEKDTKLIR 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 111 -----LELSRFTLVKLGTPPKFDKVGKGIIEKDFLVNLSDINAEQSGFLI 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 NRDKGLRDIVDTRVTKTNGDGTIDVTIVKPKQIDEGAD--VMALLDVSKMSDDF-- 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 162 RRSDDLFGYHYDTNGKN---LYDAADKFSQYFVVVDEKEVNDNISDKLTATYKKEGF 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 -----NNAKWKIKVLTKTSKASNSDNDHKLKNSVRLMTFIREI--- 287
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 218 VYGSNP-----HTKEFAARISKLG-----VEIKFENG-QAQSISKDEKGNABEIFTIKG 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 ---SNPIDISGNTES---QLDKLLDLRKKAKANYDWGVLDLQGAHKAR-----EIFNKEK 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 267 DTQKLEITPTESNRILIAILDONQKSYTPGMEKAIMETK 305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 338 EKK-----FGKRHHVLFSGESTFSYELQNSVREDX 369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 35
US-10-425-115-281772
; Sequence 281772, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 281772
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_20077C.1.pap
US-10-425-115-281772
```

```
Query Match      6.7%; Score 117; DB 17; Length 297;
Best Local Similarity 37.3%; Pred. No. 1;
Matches 31; Conservative 9; Mismatches 31; Indels 12; Gaps 1;

QY 20 LVPKTONNLQANVPQANASQANAPQANAPQANAPQANAPQANAPQANAPQANAPQAE 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 LQPOLQLHHQPOLPQVQLHSPQLQPOLVHLHPQPLPQPOLQVHQQLQQSPQVQVHEQPQ 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 VTP-----PVPQPOSQ 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 VQPBQALQSSAQQTSPQPOQAQ 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 36
US-09-815-242-5916
; Sequence 5916, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
```

```
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5816
; LENGTH: 2478
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5816
```

```
Query Match      6.7%; Score 117; DB 9; Length 2478;
Best Local Similarity 20.6%; Pred. No. 17;
Matches 83; Conservative 43; Mismatches 145; Indels 132; Gaps 16;

QY 26 NNLQANVPQ-----AQNASQANAPQANQ--APQANAPQ----- 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 983 NQVQAATTKSKDAEIAQKASERTAEAMNDSTTESQAAKQVQAVVTANADIDNA 1042
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 60 -----VENAPQANAPQVENAPQAVTPVPOPOQSKIDGSDFKI-----GSVKLNKEA-- 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1043 AANNVDNDAKTTNEATIAAITPDANVKAQAIADKYQAQOETAIDGNNGSTTEKAAAK 1102
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 109 ---QTELSRFTLVDKLGT-----PPKFDKVGSKKII-----EEKDF 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1103 QVQTEKTTADAIDAHTNAEVEAKAAIAKIEAIOPATTKDNKEATATKANERKT 1162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 143 LVNLISDINAEQLSG-----DFLIRSDDLFGYHYHTNGKNLVDAADKFSQYFVYDEK 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1163 AJAQOTDITAEIIAANAADVDNVAQTAN-----SNEAANSQNDVDOA-----K 1206
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 198 RVNDNISDKLTATYKKEGFVYGSNPHTKFEFAARISKL-----GDVEIKFEN 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1207 TTGENSIDQVTPVTKK---ATARNEITAILNNKLEIQATPDATDEKQAADAENATEN 1263
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 GOAQSGSIK-----DEKDGNAEIF-----TIKGDTKQLEITPTESNRILIA 284
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1264 GRANQAI SAATNAQVDEAKANAEEAIAINAVTPKVVKKQAQKDEIDQLQATQTN----- 1316
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 285 ILDONKSYTPGMEKAIMETKFKIDSKAGNSDKYLIIGAKSDN 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1317 VINNDQNATTEKAAIQOL-----ATAVTDAKNNTAATDQDN 1354
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 37
US-09-815-242-12967
; Sequence 12967, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Kari L.
```

; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA 011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12967  
; LENGTH: 2478  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-12967

Query Match 6.7%; Score 117; DB 9; Length 2478;  
Best Local Similarity 20.6%; Pred. No. 17;  
Matches 83; Conservative 43; Mismatches 145; Indels 132; Gaps 16;  
QY 26 NNLOAQNVPQ-----AQNAAQNAPOAQN--AFQANAPQ-----59  
Db 983 NOVQAATTKSDAKAEIACKASERKTAIEAMNDSTTEEQAAKDKVDQAVVTANADIDNA 1042  
QY 60 -----VENAPQNAQVENAPQAEVTPPVPOQSKIDGSPKI-----GSVKLANKEA-- 108  
Db 1043 AANDVDNAKTNEAIIAITPDANVPAKQAIADKVAQAEITADGNNGSTTEKAAAK 1102  
QY 109 ---QTLERSFTLVLDKLT-----PPKFDKVGSKII-----BEKDF 142  
Db 1103 QQVQTEKTADAIDAHTNAEVEAAKAAIAKIEAIQPATTTKDNAXEAIATKANERKT 1162  
QY 143 LVNLSDINAQQLSG-----DFLIRSDDLFYGYHDTNGKLVDAADKFSQYFVYVDEK 197  
Db 1163 AIAQTQDITAEIAAANADVNAVTOAN-----SNIEAANSQNDVQQA-----K 1206  
QY 198 RVNDNISDKLTATYRKKEGVYGSNPHTKFEFAARISKL-----GDVEIKFEN 244  
Db 1207 TTGENSDIQVTPVNNK---ATARNETAILNNKLOEIQATPDATDEEQAAAEANTEN 1263  
QY 245 GQAGSGIK-----DEKGNAEIP-----TIKGTKQLBITPTESNRIITA 284  
Db 1264 GKANAISATTNAQVDEAKANAEEAINAVTPKVKKQAAKDEIDQLQATQTN----- 1316  
QY 285 ILQONOKSYTPGMEKATMETKFDISKAGNSDQKYLGEAKSDN 327  
Db 1317 VINNDQNAATTEKEAIIQQL-----ATAVTDKNNITATDDN 1354

RESULT 38  
US-09-882-227-138  
; Sequence 138, Application US/09882227  
; Publication No. US20030158396A1  
; GENERAL INFORMATION:  
; APPLICANT: Kleanthous, Harold  
; APPLICANT: Al-Garawi, Amal

; APPLICANT: Miller, Charles  
; APPLICANT: Tomb, Jean-Francois  
; APPLICANT: Oomen, Raymond P.  
; TITLE OF INVENTION: Identification of Polynucleotides  
; FILE REFERENCE: Encoding No. US20030158396A1el Helicobacter Polypeptides in the  
; TITLE OF INVENTION: Genome  
; CURRENT APPLICATION NUMBER: US/09/882,227  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 08/902,615  
; PRIOR FILING DATE: 1997-07-29  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 138  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Helicobacter pylori  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 12  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-882-227-138

Query Match 5.7%; Score 116.5; DB 10; Length 298;  
Best Local Similarity 23.9%; Pred. No. 1.1;  
Matches 59; Conservative 45; Mismatches 86; Indels 57; Gaps 12;  
QY 79 EVTPFPV-----QPQSKIDGSDFKIGSVKLNKEAQT-----LELSRFTLVD----- 120  
Db 32 QITIPPLEIQEIVKILDAFTL-NTELTNTELKARKKQVYYQNMLLDFNDINQNHKD 90  
QY 121 -KLGTPPK-----FDKVSCKIIEKDFVLNLSDNAEQLSGDFLERS 164  
Db 91 AKITPKRLKTLTLAPKGVFERKLG--EVCESTNKKTKLISEVSEVKNKGMYPVINS 148  
QY 165 DDLFVGYVHDN--GKNLVDA--DKFSQYFVYDEKRVNDNISDKLTATYRKKEGVKGS 221  
Db 149 GRDLYGYHDFNDNGENITIASRGEYAGFINYFEK-----FFAGGLCYPKVKD-----T 199  
QY 222 NPHTKEFAARISKLGDVEIKFENGQAQGSIKDEKGNAEIFTIKGTKQLBITPTESNRI 281  
Db 200 NELLTKFLYFLYKLTNEIQI-MENLVFRGSI PALNKADIETLTI-----PIPPLEIQQE 251  
QY 282 IAILDQ 288  
Db 252 IVKILDQ 258

RESULT 39  
US-10-702-305A-18  
; Sequence 18, Application US/10702305A  
; Publication No. US20040213803A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael C. Chen  
; APPLICANT: Chuang-Jiun Chiou  
; APPLICANT: Zhongming Li  
; APPLICANT: Deng-Sheng Chen  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING OR  
; PREVENTING PNEUMOCOCCAL INFECTION  
; FILE REFERENCE: 12844-002001  
; CURRENT APPLICATION NUMBER: US/10/702,305A  
; CURRENT FILING DATE: 2003-11-06  
; PRIOR APPLICATION NUMBER: US 60/424,497  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 459  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polypeptide of pSA-60 PspA insert sequence  
US-10-702-305A-18

Query Match 6.7%; Score 116.5; DB 17; Length 459;  
Best Local Similarity 22.8%; Pred. No. 2;  
Matches 78; Conservative 56; Mismatches 131; Indels 77; Gaps 18;

QY 25 QNNIQ-AQNVPOAQA---SQAQNAPO-AQVAPQNAPOVENAPQNAPOAQAQVAPQAE 79  
DB 83 QSNRQISENERKKQJAEIDKEIEIAKQNLQNKQEFNKVRAEVIPEAKGLAVTKQ--KAE 140  
QY 80 VTPVPOQSQKIDGSPDKIGSVLNKEAOTLELSRF-----TL-----VDKL-- 122  
DB 141 EAKKEAEVAKRKYDYATLKVALAKKEVEAKELEIEKIQYEISTLEQEVATAQHQVDNLKX 200  
QY 123 ---GTPPKFDKVSCKKIEEKDFVLNLSINAQSLGDFLIRSDDLFYGYHDTNGKN 179  
DB 201 LLAGADPD-----DGTKVIEAK--LNKGEAELNAQAE---LAKKQTEL-----EK 241  
QY 180 LVDAADKFSQYFVYVDEKRVNDNISDKLTATYRKKEGFVYVYGNPHTKEFAARISKLGDE 239  
DB 242 LLSLDPEGKTQDELDKEAAEAEKXKADELQNKVADLEKGIAPQIKVA-----E 292  
QY 240 IKFENGQAQGSIKDEKGNABIFTIKG-----DTKQLEITPTESNRRIIAILDQNKSYT 294  
DB 293 LNKEIARLQSLKDAEENNVEDYIKEGLEQAIADKKAELATTQON-----IDTKQKD-- 344  
QY 295 PGMEKAIMETK-----FIDSKAGNSDQKYLIGEAKSD-NWQAI 331  
DB 345 --LEDAELELEKVLATLDPEGKTQDE--LDKEAAEDANIEAL 382

## RESULT 40

US-10-437-963-185221  
; Sequence 185221, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 185221  
; LENGTH: 704  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_WRT4530\_82138C.1.pep  
US-10-437-963-185221

Query Match 6.7%; Score 116.5; DB 16; Length 704;  
Best Local Similarity 20.9%; Pred. No. 3.5;  
Matches 76; Conservative 50; Mismatches 128; Indels 109; Gaps 16;

QY 6 SGGSSSTPNHPKVLVPKTONNL-----QAQNVFOAQAQA---QNAPOAQAQAQA 57  
DB 391 TCAQASTDN-VNPSDQPTGNQLAEVETAASQEPPTGQSEAGLDQBIPEVETQANVSQE 449  
QY 58 PQVENAQAQAQAPOVENAQAQVETPPVPQPOS----- 89  
DB 450 PDANDPTPGSSDKQGSFRAH-----PETSSTGLEAVRQOLHETRELAKKTEHDLRDRI 504  
QY 90 -QKIDGSPDKIGSVK-----LNKQAQTELELSRFTLVKLGTPPKFDKVSCKKIEEK 140  
DB 505 AQLQDSNPELSGSSKVQAQIAQLEKQIQTLESKTELAQAQRDSAVK--EVEDRKIKSQA 562

QY 141 DFLVLNLSINAQSLGDFLIRSDDLFYGYHDTNGKNLVDAADKFSQYFVYVDEKRVN 200  
DB 563 QPDVL-VGKIKLEGADEVANAATPLVQAMFYNNNGPSRFDAL-----VFDKLRVA 614  
QY 201 DNISDKLTATYRK--KEGFVYGSN---PHTKEFAARISKLGDEIKFENGQAQGSIKDEK 255  
DB 615 PD-----TFFKNKEAGSVGASLALAMTKSLYTKI-----DI-----DAV 649  
QY 256 DGNABIFTIKGDTKQLEITPTESNRRIIAILDQNKQS---YTPGMEKAIMETKIDSKAG 312  
DB 650 DGFAD-----RTSEVALDLINDAQAADKIAGDVYDRFQDTDLRPTGSG 694  
QY 313 NSD 315  
DB 695 NSD 697

Search completed: December 17, 2004, 16:17:59  
Job time : 178.595 secs



Db 856 SPKAPAEAPRVPEPNTPEAPHVPSFKAPBPVRVPEPNTPEAPHVPEPNTPEAPKPIE 915  
QY 72 VENAPQAEVTPVPQ-----POSQIDGSFDKIG-SVKLNKEAQTLSELSRFTLVKLG 123  
Db 916 PPKTPDVPKLPDVPKLPDAPKLPDGLNKVGOAVFTSDGNT-----KVTWV--- 967  
QY 124 TPKPKDVKSGKKIIEBKDFLVNLSDINAEOQLSGDFLIRSDDLFYGYHDTNGKLVDA 183  
Db 968 ----FDKPTDADKHLKELTKELADKIAHKTGGTV--RVFDLSL-----SKGK- 1012  
QY 184 ADKFSQVYVYDEKRVNDNISDKLTATYRKKEGFVYGSNPHTEFAARISKLGDE---I 240  
Db 1013 -----ETHVNGQRTVRLALQGTGSDVHVY-----HVKE-----NGDLERIPS 1049  
QY 241 KFEHQAGQSGIKDEKGNAEIITKGTQKLEIPTTESNRILIIALDQNKSYTPGMEKA 300  
Db 1050 KVENGQVV-----FKTNHFSFAIKTLKSDQNVTPPKQT-----KPSQTGSQVE 1093  
QY 301 IMET---KFIDSKAGN 313  
Db 1094 IASQTGKF-QSKAAN.1108

RESULT 2  
US-08-923-992A-4  
; Sequence 4, Application US/089233992A  
; Patent No. 6280738  
; GENERAL INFORMATION:  
; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Blake, Milan S.  
; TITLE OF INVENTION: No. 6280738-IGA Fc Binding Forms of the Group B  
; TITLE OF INVENTION: Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/923.992A  
; FILING DATE: 05-SEP-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024.707  
; FILING DATE: 06-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1104 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-923-992A-4

Query Match 10.3%; Score 178.5; DB 3; Length 1104;  
Best Local Similarity 24.4%; Pred.No. 2.5e-07;  
Matches 77; Conservative 43; Mismatches 119; Indels 77; Gaps 14;  
QY 12 TPNHPKPLVLPKTNLNQAVNPQAVQNAPOAQNAPQAVENAPQAVNAPOAQNAPQ 71

Db 825 SPKAPAEAPRVPEPNTPEAPHVPSFKAPBPVRVPEPNTPEAPHVPEPNTPEAPKPIE 884  
QY 72 VENAPQAEVTPVPQ-----POSQIDGSFDKIG-SVKLNKEAQTLSELSRFTLVKLG 123  
Db 885 PPKTPDVPKLPDVPKLPDAPKLPDGLNKVGOAVFTSDGNT-----KVTWV--- 936  
QY 124 TPKPKDVKSGKKIIEBKDFLVNLSDINAEOQLSGDFLIRSDDLFYGYHDTNGKLVDA 183  
Db 937 ----FDKPTDADKHLKELTKELADKIAHKTGGTV--RVFDLSL-----SKGK- 981  
QY 184 ADKFSQVYVYDEKRVNDNISDKLTATYRKKEGFVYGSNPHTEFAARISKLGDE---I 240  
Db 982 -----ETHVNGERTVRLALQGTGSDVHVY-----HVKE-----NGDLERIPS 1018  
QY 241 KFEHQAGQSGIKDEKGNAEIITKGTQKLEIPTTESNRILIIALDQNKSYTPGMEKA 300  
Db 1019 KVENGQVV-----FKTNHFSFAIKTLKSDQNVTPPKQT-----KPSQTGSQVE 1062  
QY 301 IMET---KFIDSKAGN 313  
Db 1063 IASQTGKF-QSKAAN 1077

RESULT 3  
US-08-923-992A-2  
; Sequence 2, Application US/089233992A  
; Patent No. 6280738  
; GENERAL INFORMATION:  
; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Blake, Milan S.  
; TITLE OF INVENTION: No. 6280738-IGA Fc Binding Forms of the Group B  
; TITLE OF INVENTION: Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/923.992A  
; FILING DATE: 05-SEP-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024.707  
; FILING DATE: 06-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1164 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-923-992A-2

Query Match 10.2%; Score 177; DB 3; Length 1164;  
Best Local Similarity 23.6%; Pred.No. 3.8e-07;  
Matches 81; Conservative 44; Mismatches 114; Indels 104; Gaps 15;  
QY 12 TPNHPKPLVLPKTNLNQAVNPQAVQNAPOAQNAPQAVENAPQAVNAPOAQNAPQ 71



Db 829 TPDPKIPPELPQADPTQADPTPHVPSKAPAPRVPSPKTPPEAPHVPSKAPAPR 888  
QY 72 VENAPQAEVTPVPQ----PQSKIDGSPDKIGSVKLNKEAQTLSRFTLVLDKLTGTPPK 127  
Db 889 VPESKTPPEAPHVPSKTPPEAKIP-----KPPKTPDPVKLPDPVK 936  
QY 128 -----FDKVGK---KIEBK--DFLVNLSDINAEQLSGDFLIRRS 164  
Db 937 LPDAPKLPGLNKGVAFTSTGNTKVTWFDKPTDADKHLKEVTTKELADKIA---- 992  
QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVD-----EKRVDNISDKLTATYRKKEG 216  
Db 993 -----HKTGGTV-----RVFDSLKSGKETHVNGERTVRLALGQTGSDV 1033  
QY 217 FVYGSNPHKFAARISKLGDE---IKFENGAQGSIKDEKGNABEFTIKGDTKQLEI 273  
Db 1034 HVY-----HVKE-----NGDLERIPSKVNGQV-----FKTNHFLFAIKLTSLKDNQV 1077  
QY 274 TPESNRILAILDQNKSYTPGMEKAIMET---KFIDSKAGN 313  
Db 1078 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 1108

RESULT 4  
US-08-242-932-2  
; Sequence 2, Application US/08242932  
; Patent No. 5595740  
; GENERAL INFORMATION:  
; APPLICANT: Brady, L. Jeannine  
; TITLE OF INVENTION: Cloning of No. 5595740-Iga Fc Binding Forms of  
; TITLE OF INVENTION: the Group B Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/242,932  
; FILING DATE: 16-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF142  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 984 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-242-932-2

Query Match 10.0%; Score 173; DB 1; Length 984;  
Best Local Similarity 23.3%; Pred. No. 6.8e-07;  
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;  
QY 12 TPNHKKPVLVPTQNNLQAVNQVPOAQNASOQAQNAPOAQNAPOVNAPOAQNAPO 71  
Db 649 TPDPKIPPELPQADPTQADPTPHVPSKAPAPRVPSPKTPPEAPHVPSKAPAPR 708  
QY 72 VENAPQAEVTPVPQ----PQSKIDGSPDKIGSVKLNKEAQTLSRFTLVLDKLTGTPPK 127

Db 709 VPESKTPPEAPHVPSKTPPEAKIP-----EPKTPDPVKLPDPVKLPDPVK 756  
QY 128 -----FDKVGK---KIEBK--DFLVNLSDINAEQLSGDFLIRRS 164  
Db 757 LPDAPKLPGLNKGVAFTSTGNTKVTWFDKPTDADKHLKEVTTKELADKIA---- 812  
QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVD-----EKRVDNISDKLTATYRKKEG 216  
Db 813 -----HKTGGTV-----RVFDSLKSGKETHVNGERTVRLALGQTGSDV 853  
QY 217 FVYGSNPHKFAARISKLGDE---IKFENGAQGSIKDEKGNABEFTIKGDTKQLEI 273  
Db 854 HVY-----HVKE-----NGDLERIPSKVNGQV-----FKTNHFLFAIKLTSLKDNQV 897  
QY 274 TPESNRILAILDQNKSYTPGMEKAIMET---KFIDSKAGN 313  
Db 898 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 928

RESULT 5  
US-08-714-481-2  
; Sequence 2, Application US/08714481  
; Patent No. 5766606  
; GENERAL INFORMATION:  
; APPLICANT: Brady, L. Jeannine  
; TITLE OF INVENTION: Cloning of No. 5766606-Iga Fc Binding Forms of  
; TITLE OF INVENTION: the Group B Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/714,481  
; FILING DATE: 16-SEP-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/242,932  
; FILING DATE: 16-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF142  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 984 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-714-481-2

Query Match 10.0%; Score 173; DB 1; Length 984;  
Best Local Similarity 23.3%; Pred. No. 6.8e-07;  
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;  
QY 12 TPNHKKPVLVPTQNNLQAVNQVPOAQNASOQAQNAPOAQNAPOVNAPOAQNAPO 71  
Db 649 TPDPKIPPELPQADPTQADPTPHVPSKAPAPRVPSPKTPPEAPHVPSKAPAPR 708  
QY 72 VENAPQAEVTPVPQ----PQSKIDGSPDKIGSVKLNKEAQTLSRFTLVLDKLTGTPPK 127  
Db 709 VPESKTPPEAPHVPSKTPPEAKIP-----EPKTPDPVKLPDPVKLPDPVK 756

QY 128 -----FDKVSCK---KLIBEK---DPLVLNLSDNAEOLSGDFLIRRS 164  
Db 757 LPDAPKLPDGLNKVQAVFTSTGNTKVTVVFDKPTDADKLHLKEVTTKELADKIA-----812  
QY 165 DDLFYGYHDTNGKNLVDAADKFSQYFVVYD-----EKRVNDNISDKLTATYRKKEG 216  
Db 813 -----HKTGGGT-----RVFDLSLSKGGKETHVNGERTVRLALGQTGSDV 853  
QY 217 FVYGSNPHTEFAARISKLGDVE---IKFENGQAQGSIKDEKGNABEFTIKGTQKLEI 273  
Db 854 HVY-----HVKE-----NGDLERIPSKVNGQVV-----FKTNHFSLSFAIKTLSKDQNV 897  
QY 274 TPTESNRILIIAILDQNKSYTPGMEKAIMET---KFDISKAGN 313  
Db 898 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 928  
RESULT 6  
PCT-US95-06111-2  
; Sequence 2, Application PC/TUS9506111  
; GENERAL INFORMATION:  
; APPLICANT: Street address: 186 Grinter Hall  
; APPLICANT: City: Gainesville Florida  
; APPLICANT: State/Province: US  
; APPLICANT: Country: US  
; APPLICANT: Postal code/Zip: 32611  
; APPLICANT: Phone number: 904-392-8929  
; APPLICANT: Fax number: 904-392-6600  
; APPLICANT: Telex number:  
; TITLE OF INVENTION: Cloning of Non-IgA Fc Binding Forms of  
; TITLE OF INVENTION: the Group B Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/06111  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/242,932  
; FILING DATE: 16-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UFI42  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 984 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-06111-2  
Query Match 10.0%; Score 173; DB 5; Length 984;  
Best Local Similarity 23.3%; Pred. No. 6.8e-07;  
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;  
QY 12 TPNHPKPVLPKTNLQAVNPQAVQASQANAPQANAPQAVENAPQANAPQ 71

Db 649 IPDTRFKIPELQAPDTPQAPDTPHVPESPKAPEAPRVPESEKTPPEAPHPESPAPAPR 708  
QY 72 VENAPQAEVTPVPO-----POSQIDGSFQKLGSKLNKEAQOTLESEFTLVKLTGTPPK 127  
Db 709 VPESKTPPEAPHPESPPTPEAPKIP-----EPKTPDVPKLPDVPKLPDVPK 756  
QY 128 -----FDKVSCK---KLIBEK---DPLVLNLSDNAEOLSGDFLIRRS 164  
Db 757 LPDAPKLPDGLNKVQAVFTSTGNTKVTVVFDKPTDADKLHLKEVTTKELADKIA-----812  
QY 165 DDLFYGYHDTNGKNLVDAADKFSQYFVVYD-----EKRVNDNISDKLTATYRKKEG 216  
Db 813 -----HKTGGGT-----RVFDLSLSKGGKETHVNGERTVRLALGQTGSDV 853  
QY 217 FVYGSNPHTEFAARISKLGDVE---IKFENGQAQGSIKDEKGNABEFTIKGTQKLEI 273  
Db 854 HVY-----HVKE-----NGDLERIPSKVNGQVV-----FKTNHFSLSFAIKTLSKDQNV 897  
QY 274 TPTESNRILIIAILDQNKSYTPGMEKAIMET---KFDISKAGN 313  
Db 898 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 928  
RESULT 7  
US-08-923-992A-6  
; Sequence 6, Application US/08923992A  
; Patent No. 6280738  
; GENERAL INFORMATION:  
; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Blake, Milan S.  
; TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B  
; TITLE OF INVENTION: Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/923,992A  
; FILING DATE: 05-SEP-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,707  
; FILING DATE: 06-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-923-992A-6  
Query Match 10.0%; Score 173; DB 3; Length 1128;  
Best Local Similarity 23.3%; Pred. No. 8.3e-07;  
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;  
QY 12 TPNHPKPVLPKTNLQAVNPQAVQASQANAPQANAPQAVENAPQANAPQ 71

Db 793 TPDTPKIPQLPQADPTDTPHVPSPKAPAPRVPSPKTPAPHPVPSKAPAPR 852  
QY 72 VENAPQAEVTPPVQ-----PQSQKIDGDFKIGSVKLNKEAQTLELSRFTLVLDKLTGTPPK 127  
Db 853 VPSPKTPAPHPVPSKTPAPKIP-----EPPKTPDVPKLPDVPKLPDVPK 900  
QY 128 -----FDKVSCK-----KIEEK--DPLVNLSDINAEOLSGDFLIRRS 164  
Db 901 LPDAPKLPGLNKGAVFTSTDCNTKTVVDFKPTDADKLHLKEVTTKELADKIA----- 956  
QY 165 DDLFGYHYDHTNGKLVDAADKFSQYFVVD-----EKRVDNDSKLTATYRKKEG 216  
Db 957 -----HKTGGTV-----RVFDSLSSKGGKETHVNGERTVRLALGQTGSDV 997  
QY 217 FVYGSNPHKFEARISKLGDE-----IKFENGQAQGSIKDEKGNABIFTIKGDTKOLEI 273  
Db 998 HVY-----HVKE-----NGDLERIPSKVGVV-----FKTNHPSLFAIKTSLKQNV 1041  
QY 274 TPTESNRIIIAILDONQKSYTPGMEKAIMET---KFDISKAGN 313  
Db 1042 TPKQT-----KPTQSGQVEIAESQTGKF-QSKAAN 1072

RESULT 8  
US-08-923-992A-8  
; Sequence 8, Application US/08923992A  
; Patent No. 6280738  
; GENERAL INFORMATION:  
; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Blake, Milan S.  
; TITLE OF INVENTION: No. 6280738-IGA Pc Binding Forms of the Group B  
; TITLE OF INVENTION: Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/923,992A  
; FILING DATE: 05-SEP-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,707  
; FILING DATE: 06-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2500  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1098 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-923-992A-8

Query Match 9.7%; Score 168; DB 3; Length 1098;  
Best Local Similarity 23.0%; Pred. No. 2.3e-06;  
Matches 79; Conservative 45; Mismatches 115; Indels 104; Gaps 15;  
QY 12 TPNHFKPVLVPTQNNLQNVQVQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71

Db 792 TPDTPKIPQLPQADPTDTPHVPSPKAPAPRVPSPKTPAPHPVPSKAPAPR 851  
QY 72 VENAPQAEVTPPVQ-----PQSQKIDGDFKIGSVKLNKEAQTLELSRFTLVLDKLTGTPPK 127  
Db 852 VPSPKTPAPHPVPSKTPAPKIP-----EPPKTPDVPKLPDVPKLPDVPK 899  
QY 128 -----FDKVSCK-----KIEEK--DPLVNLSDINAEOLSGDFLIRRS 164  
Db 900 LPDAPKLPGLNKGAVFTSTDCNTKTVVDFKPTDADKLHLKEVTTKELADKIA----- 955  
QY 165 DDLFGYHYDHTNGKLVDAADKFSQYFVVD-----EKRVDNDSKLTATYRKKEG 216  
Db 956 -----HKTGGTV-----RVFDSLSSKGGKETHVNGERTVRLALGQTGSDV 996  
QY 217 FVYGSNPHKFEARISKLGDE-----IKFENGQAQGSIKDEKGNABIFTIKGDTKOLEI 273  
Db 997 HVY-----HVKE-----NGDLERIPSKVGVV-----FKTNHPSLFAIKTSLKQNV 1040  
QY 274 TPTESNRIIIAILDONQKSYTPGMEKAIMET---KFDISKAGN 313  
Db 1041 TPKQT-----KPTQSGQVEIAESQTGKF-QTKAAN 1071

RESULT 9  
US-08-515-251A-2  
; Sequence 2, Application US/08515251A  
; Patent No. 5891677  
; GENERAL INFORMATION:  
; APPLICANT: GERLACH, GERALD F.  
; APPLICANT: WILLSON, PHILIP J.  
; APPLICANT: ROSSI-CAMPOS, AMALIA  
; APPLICANT: POTTER, ANDREW A.  
; TITLE OF INVENTION: ACTINOBACILLUS PLEUROPEUMONIAE OUTER  
; MEMBRANE LIPOPROTEIN A AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: ROBINS & ASSOCIATES  
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/515,251A  
; FILING DATE: 15-AUG-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/971,558  
; FILING DATE: 05-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINS, ROBERTA L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 9001-0027.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 325-7812  
; TELEFAX: (650) 325-7823  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 365 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-515-251A-2

Query Match 9.2%; Score 159.5; DB 2; Length 365;  
Best Local Similarity 24.1%; Pred. No. 2.7e-06;  
Matches 92; Conservative 54; Mismatches 139; Indels 97; Gaps 21;

QY 1 CGSGSGSSSTPNHPKFLVLPKTONNQVPOAQNASQAQNAPOAQNAPOAQN----- 56  
Db 20 CGSGSGSSSSKPNSE---LTPKVD-----MSAPKAEQ-----PKKEVPQADNSKAE 64  
QY 57 -----APQVENAPOAQN-----APQVENA-----PQAEVTPVPVPOQSQKIDGSPKIGSVK 103  
Db 65 BKEVAPQVD-SPKAEPRNNAPQGNPKLNDPQV-NAPKMDNFQKAPKGE-----E 115  
QY 104 LNKEAQTELSRFTLVKX--GTPPKFKVSGKKIIEKFL--VLNLSDNAEQLSGDF 159  
Db 116 LSKDSKNAEILKELGVKDGINSIINNADVLNLK-IDEKDHTVLDKGINRHILKVTN 174  
QY 160 LIRRSDDLFGYHHTGKNLVDAAKFSQY--FVVYDEKRVNDNISDKLTATYRKKEGF 217  
Db 175 TISAQDI-----KTLKDSGKLLGYGYMQLNQVRQDENYSDEKVS-----E 220  
QY 218 VYGSNPHTKFAAR--ISKLGVEIKFE--NGOAGSGIKDEKGNAEIFTIK----- 265  
Db 221 LLSMNDADKIRPTKISYKGMFYSYKDVGNQKLSASVEASYDDVTYKVMKVGENDY 280  
QY 266 -----GDTKLEIPTTES-----NRIIAILDQNKSYTPGMEKAIMETKFDISK 310  
Db 281 WKLGFRGTNLLENQVTKAKVGEDGTINGTLYSKIDNFPKLT-----DANFSGGI 333  
QY 311 AGNSDKYLLIGKSNWQAIM 332  
Db 334 FKNGE-VLAGSAISERKQWGI 354

## RESULT 10

US-08-515-251A-4  
; Sequence 4, Application US/08515251A  
; Patent No. 5891677  
; GENERAL INFORMATION:  
; APPLICANT: GERLACH, GERALD F.  
; APPLICANT: WILLSON, PHILIP J.  
; APPLICANT: ROSSI-CAMPOS, AMALIA  
; APPLICANT: POTTER, ANDREW A.  
; TITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEUMONIAE OUTER  
; TITLE OF INVENTION: MEMBRANE LIPOPROTEIN A AND USES THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBINS & ASSOCIATES  
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/515.251A  
; FILING DATE: 15-AUG-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/971,558  
; FILING DATE: 05-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINS, ROBERTA L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 9001-0027.10  
; TELEPHONE: (650) 325-7812  
; TELEFAX: (650) 325-7823  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 367 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-515-251A-4  
Query Match 8.0%; Score 138.5; DB 2; Length 367;  
Best Local Similarity 22.1%; Pred. No. 0.00022;  
Matches 91; Conservative 61; Mismatches 105; Indels 155; Gaps 26;  
QY 1 CGSGSGSSSTPNHPKFLVLPKTONNQVPOAQNASQAQNAPOAQN-----APQAN 56  
Db 20 CGSGSGSSSPKPNSES---TPKVDMSAPKAPQPKKEAPQA-DSPKAEKPKSIAPLWME 75  
QY 57 APQVENAPOAQNAPOAQNAPOA---EVTTP---VPQSQKIDGSGFK----- 98  
Db 76 NPKVEK--QRENLO--EKSPKADPEQVMDPKLGAPQKDDQKLEEPKNSNAEILKELGK 132  
QY 99 -----IGSVKLKNEAQTLELSRFTLV-----DKLGTTPPKFKVSGKKIIEK--- 141  
Db 133 DITSGTISISDIELNLQLDSDNVDNVLNENLMDNLIN---NKIAGSDIRTLKDSGG 189  
QY 142 -----FLVLN-----LSDNAEQLSGDFLIRRSDDLFGYH 173  
Db 190 RLLGYGYVQLNQVTDQSRDPNPKHFENHYLLSMNDAEKILPEKSLYKGMTYGY-- 247  
QY 174 DTNGKNLVDAAKFSQYFVVYDEKRVNDNISDKLTATYRKKEGFVYGSNPHTKFAARIS 233  
Db 248 NTSG-----NEKLTAEVNAK-----YDSS--TKLSMKVY 275  
QY 234 -----KJGDV---EIKFENGQAQSIKDEKDG--NAEIFTIKGTKOLEITPTESNRII 282  
Db 276 DNDRYWKLGEVMSNNVRLPEEKVDG-VKVDSDGTINARLYL--STEEPLKLT----- 325  
QY 283 IAILDQNKSYTPGMEKAIMETKFDISKAGNSDKYLLIGKAS--DNWQAIM 332  
Db 326 ----DAN---FSGG-----IFGKNG-----EVLAKGAESIKGEWQWGI 356

## RESULT 11

US-08-155-888-2  
; Sequence 2, Application US/08155888  
; Patent No. 6066623  
; GENERAL INFORMATION:  
; APPLICANT: Hoffman, Stephen L.  
; APPLICANT: Hedstrom, Richard C.  
; APPLICANT: Sedegah, Martha  
; TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE PROTECTIVE  
; TITLE OF INVENTION: AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR  
; TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.  
; STREET: Bldg. 1, T-12 8901 Wisconsin Ave.  
; CITY: Bethesda  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20889-5606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/155.888  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spevack, A. David  
; REGISTRATION NUMBER: 24,743  
; REFERENCE/DOCKET NUMBER: N.C. 75.851  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 295-6759  
; TELEFAX: (202) 295-1022  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-155-888-2

Query Match      7.6%; Score 131; DB 3; Length 478;
Best Local Similarity 36.0%; Pred. No. 0.0016;
Matches 32; Conservative 3; Mismatches 54; Indels 0; Gaps 0;

QY  2 GSGSGSSSTNHPKVLVPTQNNLQAVNPQAQNASQAQNAPOAQAQNAPOVE 61
Db  265 GAPQGGAPQGGAPQGGAPQGGAPQGGAPQGGAPQGGAPQGGAPQGGAPQ 324

QY  62 NAPQAQNAQVENAPQAEVTPVPQPSQ 90
Db  325 GAPQGGAPQGGAPQGGAPQGGAPQGGAPQGGAPQGGAPQGGAPQ 353

RESULT 12
US-08-749-391-2
; Sequence 2, Application US/08749391
; Patent No. 5948667
; GENERAL INFORMATION:
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Selinger, Leonard B.
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Hu, Youji
; APPLICANT: Forsberg, Cecil W.
; APPLICANT: Moloney, Maurice M.
; TITLE OF INVENTION: A Xylanase Obtained From an
; TITLE OF INVENTION: Anaerobic Fungus
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80803
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,391
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna M. Ferber
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 93-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-391-2

Query Match      7.3%; Score 127; DB 2; Length 485;
Best Local Similarity 36.8%; Pred. No. 0.0038;
Matches 35; Conservative 10; Mismatches 44; Indels 6; Gaps 4;

QY  2 GSGSGSSSTNHPKVLVPTQNNLQAVNPQAQNASQAQNAPOAQAQNAPOVE 61
Db  256 GGAPAGGAPAGNDQPG---PQGQPPQGGQPPQGGQPPQGGQPPQGG-NDQGGQ 311

QY  62 NAPQAQNAQVENAPQAEVTPVPQ-PQSQKIDGS 95
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Db  312 QPPQGGQPPQGGQPPQGGQPPQGGQPPQGGQPPQGGQPPQGGQPPQGG 345

RESULT 13
US-09-390-200-2
; Sequence 2, Application US/09390200
; Patent No. 6137032
; GENERAL INFORMATION:
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Selinger, Leonard B.
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Hu, Youji
; APPLICANT: Forsberg, Cecil W.
; APPLICANT: Moloney, Maurice M.
; TITLE OF INVENTION: A Xylanase Obtained From an
; TITLE OF INVENTION: Anaerobic Fungus
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80803
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/390,200
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,391
; FILING DATE: 13-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna M. Ferber
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 93-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-390-200-2

Query Match      7.3%; Score 127; DB 3; Length 485;
Best Local Similarity 36.8%; Pred. No. 0.0038;
Matches 35; Conservative 10; Mismatches 44; Indels 6; Gaps 4;

QY  2 GSGSGSSSTNHPKVLVPTQNNLQAVNPQAQNASQAQNAPOAQAQNAPOVE 61
Db  256 GGAPAGGAPAGNDQPG---PQGQPPQGGQPPQGGQPPQGGQPPQGG-NDQGGQ 311

QY  62 NAPQAQNAQVENAPQAEVTPVPQ-PQSQKIDGS 95

Db  312 QPPQGGQPPQGGQPPQGGQPPQGGQPPQGGQPPQGGQPPQGGQPPQGG 345

RESULT 14
US-08-487-890A-115
; Sequence 115, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
```

APPLICANT: Chong, Pele  
 APPLICANT: Gray-Owen, Scott  
 APPLICANT: Yang, Yan-Ping  
 APPLICANT: Murphy, Andrew  
 APPLICANT: Klein, Michel  
 TITLE OF INVENTION: Transferrin Receptor Genes  
 NUMBER OF SEQUENCES: 147  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: 6th Floor, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,890A  
 FILING DATE: 07-JUN-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/175,116  
 FILING DATE: 29-DEC-1993  
 APPLICATION NUMBER: US 08/148,968  
 FILING DATE: 08-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-466 MIS:jfb  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 115:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 631 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-487-890A-115

Query Match	7.23;	Score 124;	DB 1;	Length 631;
Best Local Similarity	24.03;	Pred. No. 0.01;		
Matches	67;	Conservative 44;	Mismatches 98;	Indels 70; Gaps 14;
QY	72	VENAQAQAEVTPPVQPOQ-----SQIDGSFDKIGSVKLNKEAQTLELSRFTLVDKL	122	
Db	322	VFSAKETEERPKLPKETLIDGKLTTSKTTDTTNNKTTSAKNTS-----NFTKD--	372	
QY	123	GTPKPKFVKVSGKKIIEKDFVLNLSIDIAEQSLGDFLIRRSDDLFCYYHYDHTGKML-V	181	
Db	373	--IPSGF-----EADYLLIDNYPILPLPESGDFISSK-----HHEVGGKRYK	413	
QY	182	DAADK---FSQYFVYDEKVDNIDSK-----LATATYRKKEGFVYGSNPHTKEFAARIS	233	
Db	414	EACCKNLCCYKFGMYEDKKNKNNTDKEKQTTTSIKTYQPLGLRLTSPSE---IP	469	
QY	234	KLGDVLEIKFNGQAQGSIKDEKQGNAEIETIKGDIKQLEITPTESNRILIIAILDQNKSY	293	
Db	470	KMGNVYTR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAFN-----ADFNKKL	516	
QY	294	TPGMEKAIMETKFIDSKA-----GNSDQKYLIGEAKSNNW	328	
Db	517	TGTSKRHDNPVPFNIKATPONGRNDPE---GTATAENF	552	

RESULT 15  
US-08-478-435-115  
; Sequence 115, Application US/08478435  
; Patent No. 5922323

```

; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,435
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-462 M15:Vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-478-435-115

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Query Match	7.2%	Score 124;	DB 2;	Length 631;
Best Local Similarity	24.0%;	Prod. No. 0.01;		
Matches 67;	Conservative 4%;	Mismatches 98;	Indels 70;	Gaps 14;
QY	72	VENAFOAEVTPVPPO-	-----SQIDGSFDKIGSVKLNKEAQTLELSRFTLVDKL	122
DB	322	VFSAKETFEKPKPELIDGLKLTTSKTDITTNKTTSAKNT-	-----NFTKD-	372
QY	123	GTPPKFKVSGKKIIEBKDFVLNLSDDINAEQLSGDFLIERSDDLFGYVYHDTNGNL-V	181	
DB	373	-IPSG-----EADYLLIDNPYIPLPESGDFISSK-----HHEVGGRYKV	413	
QY	182	DAADK-----FSQYFVVDYKRWNDNIDK-----LTATYRKKEGFGVGSNPHTKEFAARIS	233	
DB	414	EACCKNLVYKFGMYEDKENNKNETDKERKQTTISIKTYQFLGLLTPSSE-----IP	469	
QY	234	KLGDVETKFNQAQSGIKDEKCGNAEITIKGDTKQLEITPTESNRILIIAILDQNKSY	293	
DB	470	KMGVNTYR-----GSWFGYIGDQKTS-----YSATGDRQDKNAPAEF-	516	
QY	294	TPGMEKAIMETKFDLSKA-----GNSDOKYLIIEAKSDNW	328	

Db 517 TGTSKRHDNQNPVFNKATFQNGRDNFE---GTATAENF 552

## RESULT 16

US-08-337-483-115

; Sequence 115, Application US/08337483

; Patent No. 5922562

; GENERAL INFORMATION:

; APPLICANT: Loosmore, Sheena

; APPLICANT: Harkness, Robin

; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele

; APPLICANT: Gray-Owen, Scott

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Murdin, Andrew

; APPLICANT: Klein, Michel

; TITLE OF INVENTION: Transferrin Receptor Genes

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sim & McBurney

; STREET: Suite 701, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1R7

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/337,483

; FILING DATE: 08-NOV-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Stewart, Michael I

; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 595-1155

; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 115:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 631 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-337-483-115

Query Match 7.2%; Score 124; DB 2; Length 631;

Best Local Similarity 24.0%; Pred. No. 0.01;

Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPVPQPOQ-----SOKIDGDFKIGSVKLNKEAQTLELSRFTLVYDKL 122

Db 322 VFSKETEERKPLPKETLIDGKLTFTSKTDTTNTKTSKNTNTE-----NFTTKD-- 372

QY 123 GTPPKDFKVSCKKIEEKDFLVNLSDINAEQLSGDFLIIRSDDLFVGYVHDTNGKNL-V 181

Db 373 --IPSG-----EADYLLIDNVPILPLPSGDFISSK-----HHEVGGRKYV 413

QY 182 DAADK---FSQYFVYVDEKRVNDNISDK-----LTATYRKKEGFVYGSNPHTKFAARIS 233

Db 414 EACCKNLGVKFGMYEDKENNKNETDKEKEKQTTTSIKTYQFLGLRTPSE-----IP 469

QY 234 KLGDVEIKFNGQAQSGIKDEKGNAEIFIKGDTKQLEITPTESRIIAILDQNKSY 293

Db 470 KVGNVYR---GSGWFGYIGDKTS-----YSATGDKQDKKNAPAEFN-----ADFNKKL 516

QY 294 TPGMEKAIMETKPIDSKA-----GNSDQKYLIGBAKSDNW 328

Db 517 TGTSKRHDNQNPVFNKATFQNGRDNFE---GTATAENF 552

## RESULT 17

US-08-478-373-115

; Sequence 115, Application US/08478373

; Patent No. 5922841

; GENERAL INFORMATION:

; APPLICANT: Loosmore, Sheena

; APPLICANT: Harkness, Robin

; APPLICANT: Schryvers, Anthony

; APPLICANT: Chong, Pele

; APPLICANT: Gray-Owen, Scott

; APPLICANT: Yang, Yan-Ping

; APPLICANT: Murdin, Andrew

; APPLICANT: Klein, Michel

; TITLE OF INVENTION: Transferrin Receptor Genes

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sim & McBurney

; STREET: Suite 701, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1R7

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/478,373

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/337,483

; FILING DATE: 08-NOV-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/175,116

; FILING DATE: 29-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/148,968

; FILING DATE: 08-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Stewart, Michael I

; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 595-1155

; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 115:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 631 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-478-373-115

Query Match 7.2%; Score 124; DB 2; Length 631;

Best Local Similarity 24.0%; Pred. No. 0.01;

Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPVPQPOQ-----SOKIDGDFKIGSVKLNKEAQTLELSRFTLVYDKL 122

Db 322 VFSKETEERKPLPKETLIDGKLTFTSKTDTTNTKTSKNTNTE-----NFTTKD-- 372

QY 123 GTPPKDFKVSCKKIEEKDFLVNLSDINAEQLSGDFLIIRSDDLFVGYVHDTNGKNL-V 181

Db 373 --IPSG-----EADYLLIDNVPILPLPSGDFISSK-----HHEVGGRKYV 413

QY 182 DAADK---FSQYFVYVDEKRVNDNISDK-----LTATYRKKEGFVYGSNPHTKFAARIS 233

Db 414 EACCKNLGVKFGMYEDKENNKNETDKEKEKQTTTSIKTYQFLGLRTPSE-----IP 469

QY 234 KLGDEVEIKFENGQAGSISKDEKGNABIFITIKGTQKLEITPTESNRILIIAILDONOKSY 293  
DB 470 KMGNTYR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAEFN-----ADFNKKL 516

QY 294 TPGMEKAIMETKFIDSKA---GNSDQKYLIGEAKSDNW 328  
DB 517 TGTSGRHDNQNPVNIKATFQNGRNDPE---GTATAENF 552

RESULT 18  
US-08-474-671-115  
; Sequence 115, Application US/08474671  
; Patent No. 6008326  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-ping  
; APPLICANT: Murdin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: Suite 701, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,671  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/337,483  
; FILING DATE: 08-NOV-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,116  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/148,968  
; FILING DATE: 08-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 631 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-474-671-115

Query Match 7.28; Score 124; DB 3; Length 631;  
Best Local Similarity 24.08; Pred. No. 0.01;  
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPVPQPOQ-----SOKIDGSFDKIGSVKLNKEAQTLELSFTLVDKL 122  
DB 322 VFSKETEERKPKPKEITLIDGLKLTFTSKTTDTTNTKTTSKNTTE-----NFTTKD-- 372

QY 123 GTTPEKDKVSGKKIIEKDFLVNLSDINABQLSGDFLIRSDDLFYGYHYHTWCKNL-V 181  
DB 373 --IPSG-----EADYLLIDNYPILPLPESGDFISSK-----HHEVGGRYKV 413

QY 182 DAADK---FSQVYVYDEKRVNDNISDK-----LTATYRKEKEGFYVGSNPHTKFAARIS 233  
DB 414 EACCKNLGVKFGMYEYEDKENNKNETDKEKEQTTSIKTYVQFLGLLRTPSSE---IP 469

QY 234 KLGDEVEIKFENGQAGSISKDEKGNABIFITIKGTQKLEITPTESNRILIIAILDONOKSY 293  
DB 470 KMGNTYR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAEFN-----ADFNKKL 516

QY 294 TPGMEKAIMETKFIDSKA---GNSDQKYLIGEAKSDNW 328  
DB 517 TGTSGRHDNQNPVNIKATFQNGRNDPE---GTATAENF 552

RESULT 19  
US-08-483-577A-115  
; Sequence 115, Application US/08483577A  
; Patent No. 6015668  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-ping  
; APPLICANT: Murdin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 160  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: Suite 701, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,577A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/337,483  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,116  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/148,968  
; FILING DATE: 08-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-511  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 115:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 631 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-577A-115



Query Match 7.2%; Score 124; DB 3; Length 631;  
Best Local Similarity 24.0%; Pred. No. 0.01;  
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;  
US-08-897-438-115  
QY 72 VENAPQAEVTPVPQPOQ-----SOKIDGSPDKIGSVKLNKEAQTLELSRFTLVDKL 122  
Db 322 VFSKETEKEPKLPKRETLIDGKLTFTSKTDTTNTKTSKNTTE-----NFTTKD-- 372  
QY 123 GTPPKFDKVSCKKIEBKDFLVNLSDINAEQSGDFLIRSDDLFGYHYHTNGKML-V 181  
Db 373 --IPSPFG-----EADYLLIDNYPIPLLPESGDFISSK-----HHEVGGKRYKV 413  
QY 182 DAADK---FSQYFVYDEKRVNDISDK-----LTATYRKKEGFFVYGSNPHTKFAAARIS 233  
Db 414 EACCKNLCYVKFGMYEDKENNKVETDKEKEKQTTTSIKTYQFLGLRTPSE-----IP 469  
QY 234 KLGDEVEIKFENGQAQGSIKDEKGNABEFTIKGDTKQLEITPTESNRHIIAILDQNKSY 293  
Db 470 KMGNTYR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAEFN-----ADFNKKL 516  
QY 294 TPGMEKAIMETKFIDSKA-----GNSDKYLIKEAKSDNW 328  
Db 517 TGTSKRHDNQNPVFNKATFQNGRDNDFE---GTATAENF 552  
RESULT 20  
US-08-897-438-115  
; Sequence 115, Application US/08897438  
; Patent No. 6262016  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena  
; APPLICANT: Harkness, Robin  
; APPLICANT: Schryvers, Anthony  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Murdin, Andrew  
; APPLICANT: Klein, Michel  
; TITLE OF INVENTION: Transferrin Receptor Genes  
; NUMBER OF SEQUENCES: 160  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/897,438  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/483,577.  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/337,483  
; FILING DATE: 08-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/175,116  
; FILING DATE: 29-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,968  
; FILING DATE: 08-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-720  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 631 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-897-438-115  
Query Match 7.2%; Score 124; DB 3; Length 631;  
Best Local Similarity 24.0%; Pred. No. 0.01;  
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;  
US-08-897-438-115  
QY 72 VENAPQAEVTPVPQPOQ-----SOKIDGSPDKIGSVKLNKEAQTLELSRFTLVDKL 122  
Db 322 VFSKETEKEPKLPKRETLIDGKLTFTSKTDTTNTKTSKNTTE-----NFTTKD-- 372  
QY 123 GTPPKFDKVSCKKIEBKDFLVNLSDINAEQSGDFLIRSDDLFGYHYHTNGKML-V 181  
Db 373 --IPSPFG-----EADYLLIDNYPIPLLPESGDFISSK-----HHEVGGKRYKV 413  
QY 182 DAADK---FSQYFVYDEKRVNDISDK-----LTATYRKKEGFFVYGSNPHTKFAAARIS 233  
Db 414 EACCKNLCYVKFGMYEDKENNKVETDKEKEKQTTTSIKTYQFLGLRTPSE-----IP 469  
QY 234 KLGDEVEIKFENGQAQGSIKDEKGNABEFTIKGDTKQLEITPTESNRHIIAILDQNKSY 293  
Db 470 KMGNTYR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAEFN-----ADFNKKL 516  
QY 294 TPGMEKAIMETKFIDSKA-----GNSDKYLIKEAKSDNW 328  
Db 517 TGTSKRHDNQNPVFNKATFQNGRDNDFE---GTATAENF 552  
RESULT 21  
US-08-637-654-115  
; Sequence 115, Application US/08637654  
; Patent No. 6358727  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M  
; APPLICANT: Harkness, Robin E  
; APPLICANT: Schryvers, Anthony B  
; APPLICANT: Chong, Pele  
; APPLICANT: Gray-Owen, Scott  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Murdin, Andrew D  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/637,654  
; FILING DATE: 05-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/CA94/00616  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-595

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-637-654-115

Query Match          7.2%; Score 124; DB 3; Length 631;
Best Local Similarity 24.0%; Pred. No. 0.01;
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPVPQPOQ-----SQKIDGSPDKIGSVKLNKEAQTLELSRFTLVDKL 122
DB 322 VFSKETEELPKPKETLIDGKLTFTSKTTDTTNTKTSKNTNTE-----NFTTKD-- 372
QY 123 GTPPKFDKVSCKIIEEKDFLVNLSDINAEQLSGDFLIRSDDLFYGYVHDTNGKIL-V 181
DB 373 --IPSFG-----EADYLLIDNYPIPLPESGDFISSK-----HHEVGKRYKV 413
QY 182 DAADK---FSQYFVYDEKRVNDNISK-----LTATYRKKEGFGVGSNPHTEFAARIS 233
DB 414 EACCKNLGVKFGMYEDKKNKNETDKEREKQTTTSIKTYQFLLGLRTPSSE---IP 469
QY 234 KLGVEIKFENGQAQGSIKDEKGNAEFTIKGPTKOLEITPTESNRIIAILDQOKSY 293
DB 470 KMGNTVYR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAEFN-----ADFNKKL 516
QY 294 TPGMEKAIMETKFDISKA-----GNSDQKYLIGEAKSDNW 328
DB 517 TGTSKRHDNQNPVENIKATFONGRDNFE---GTATAENF 552

RESULT 22
US-08-649-518-115
; Sequence 115, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murgin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Slim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/649,518
; APPLICATION NUMBER: US/08/649,518
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-649-518-115

Query Match          7.2%; Score 124; DB 3; Length 631;
Best Local Similarity 24.0%; Pred. No. 0.01;
Matches 67; Conservative 44; Mismatches 98; Indels 70; Gaps 14;

QY 72 VENAPQAEVTPVPQPOQ-----SQKIDGSPDKIGSVKLNKEAQTLELSRFTLVDKL 122
DB 322 VFSKETEELPKPKETLIDGKLTFTSKTTDTTNTKTSKNTNTE-----NFTTKD-- 372
QY 123 GTPPKFDKVSCKIIEEKDFLVNLSDINAEQLSGDFLIRSDDLFYGYVHDTNGKIL-V 181
DB 373 --IPSFG-----EADYLLIDNYPIPLPESGDFISSK-----HHEVGKRYKV 413
QY 182 DAADK---FSQYFVYDEKRVNDNISK-----LTATYRKKEGFGVGSNPHTEFAARIS 233
DB 414 EACCKNLGVKFGMYEDKKNKNETDKEREKQTTTSIKTYQFLLGLRTPSSE---IP 469
QY 234 KLGVEIKFENGQAQGSIKDEKGNAEFTIKGPTKOLEITPTESNRIIAILDQOKSY 293
DB 470 KMGNTVYR---GSWFGYIGDDKTS-----YSATGDKRQDKNAPAEFN-----ADFNKKL 516
QY 294 TPGMEKAIMETKFDISKA-----GNSDQKYLIGEAKSDNW 328
DB 517 TGTSKRHDNQNPVENIKATFONGRDNFE---GTATAENF 552

RESULT 23
US-09-270-767-43054
; Sequence 43054, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43054
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43054

Query Match          7.0%; Score 121; DB 4; Length 808;
Best Local Similarity 28.1%; Pred. No. 0.028;
Matches 56; Conservative 22; Mismatches 63; Indels 58; Gaps 12;

QY 15 HPK-----PVLVPKTONNLQANVP-----CAQNASQAQNAQ-----QAQNAPO 53
DB 307 HPQKQQTTPPAPQTPGTYVYRTPIFVEGSEPIINAHKEIPNQAPPSPAQAQAQAY 366
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QY 54 AQAPOVNAPOAQAPOVNA-POAEVTPPV-OPQSQKIDGSPDKIGSVKLNKE 107  
Db 367 AQAQVQVHAAPQOHNPPTLNTQPSQEQVVEGAAGLPQTPHLSINKIQDI---Q 422  
QY 108 AOTLESLRRTLVDKLTGTPPKVSKKIIIEKDFLVNLSDINAEQLSGDFLIRSDLL 167  
Db 423 RDVLEL-----MG---KVEQFKGTR--BEKEYAYLD-----EMLTRNL--KLPTI 461  
QY 168 FYGYHDTNGKLVDAADK 186  
Db 462 -----DTNGKDSIRLARK 474

RESULT 24  
US-09-134-000C-6588  
; Sequence 6588, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 6588  
; LENGTH: 1308  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
; US-09-134-000C-6588

Query Match 7.0%; Score 121; DB 4; Length 1308;  
Best Local Similarity 19.4%; Pred. No. 0.057;  
Matches 85; Conservative 59; Mismatches 157; Indels 138; Gaps 18;

QY 3 GSGSGSSSTPNHPKPVLPKTONNLOAQNVP-----QAQNASQON-APQQA 49  
Db 98 GTAAEQSSATSDNTTNNQOPTAEAKSAQEQPVVSPETTIEPLGQPTVAPAEANDANKST 157  
QY 50 NAPQAQNAPOVNA-POAQAPOV-ENAPQAEVTPPVQPOSQKI 92  
Db 158 SIPKEFETPDVKAQVDEAKDPNITVEXPTEDLGNVSSKDLAAKEVDQLQKEQAQKI 217  
QY 93 -----DGSFDKIGSV-----KLNKEAQTLELSRF----- 116  
Db 218 AQAQAEELKAKNEKIATKENAEIAAKNAEKERYEKEVAEYNKHNKNDKGYVNEAISKDLVFD 277  
QY 117 -TLVDKLTGTPPKVSKKIIIEKDFLVNLSDINAEQLSGDFLIRSDLLFYGYHDT 175  
Db 278 SSIVTK---DTKIDKITGGKFIKASDFNKVNOG-----QSKDIFTKLSKDM 320  
QY 176 NGK-----NLVDAADKFSQYFVYVDEKEVDNIDKLTATY--RK--KEGFVYGS 221  
Db 321 NGKATGNFQSSKYSVAVEFGPKGGVAVLEKNKPNVITYTG-LNASYLNKRIKABEIIY-- 377  
QY 222 NPHTEFAAIRISKLGDEVEIKFENGQAQGSIKDEKGNAE-----IFTIK-GDTKQLEIIFT 276  
Db 378 -----ELQSAFQSGSLNVAFSDPIITAFVGTKNANGKDKVRLTIKLYDANGKEVLPE 432  
QY 277 ESNRIIITAILDQKQSYTPGMKAEIMETKIDSKAGNSDOKYLIGE----- 322  
Db 433 KDAFAFALSLSNS---SLGTNYSVEHAEPVSDFGSKNEFKYINGSVYVKKQADKKEYSTE 489  
QY 323 -----AKSDNWOAI 331  
Db 490 DLDVGTGPGSLKNSDWDV 508

RESULT 25

US-08-750-152A-2  
; Sequence 2, Application US/08750152A  
; Patent No. 5977331  
; GENERAL INFORMATION:  
; APPLICANT: ASAKURA, YOKO  
; APPLICANT: KIMURA, EIICHIRO  
; APPLICANT: ABE, CHIZU  
; APPLICANT: KAWAHARA, YOSHIO  
; APPLICANT: NAKAMATSU, TSUYOSHI  
; TITLE OF INVENTION: ALPHA-KETOGLUTARATE DEHYDROGENASE GENE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22152  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/750,152A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NORMAN P. OBLON  
; REGISTRATION NUMBER: 24,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1257 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-750-152A-2

Query Match 6.7%; Score 116.5; DB 2; Length 1257;  
Best Local Similarity 22.1%; Pred. No. 0.14;  
Matches 91; Conservative 54; Mismatches 121; Indels 145; Gaps 24;

QY 7 GGSSTPNHPKPVLPKTONNLOAQNVPQAQNASQAQNAPOAQAPOAQAPOVNAPOA 66  
Db 76 GGNATP-----ATTEAQ--PSAPKES-AKPAKPA--APAAKAAPRVETKPA 118  
QY 67 QNAPQVE--NAPQAEVTPPVQPOSQKIDGSPDKIG-SVKLNKEAQTLE----- 111  
Db 119 KTAFAKKESSVQ--QPKLPEPGQTPIRGIFKSIKAKMDISLEIPTSATSVDMPARLMF 175  
QY 112 -----ELSR-----FTLVKLTGTPP-----KFDKVSQKKIIEKDFLVN 146  
Db 176 ENRAMVNDOLKTRGKGIKSFTHIIGYAMVKAHMAHPDMNNSYDVIDGKPTLIVPEHNLG 235  
QY 147 LSDINAEQLSGDFLIRSDLLFYGYHDTNGKLVDAADK-----FSQYFVYVDEKVN 200  
Db 236 LA-IDLPQKDG-----SRALVVAIKETKKNFSEFLAAY-EDIVT 274  
QY 201 DNISDKLTATYRKKEGFVYG-SNP---HTKEFAAIRSK-----LGDVEIKFENGQAQ 249  
Db 275 RSRKGLTMD--DYQGVTVSLTNGGIGTRHVSFRLTKGQGTIIIGVSGMDYPAE---PQ 329  
QY 250 SIKDEKGNABEIFTKGTQKLEITPTESNRILIA-----ILD 287  
Db 330 ASEDRL---AEL-----GVGKLVITITSTYDHRVIOGAVSGEFLRTMSRLLLTDSFWEI 382  
QY 288 QNQSXYTP-----GMEKAIMETKIDSKAGNSDQKYLIGEAKSDNW 328

Db 393 AMNVPYPMRWAQDPVNTGVDKNTRVQMLIEAYRSRG---HLIADTNPLSW 430  
Query Match 6.7%; Score 115.5; DB 4; Length 881;  
Best Local Similarity 22.9%; Pred. No. 0.1;  
Matches 66; Conservative 34; Mismatches 83; Indels 105; Gaps 14;

## RESULT 26

US-09-486-072-2  
; Sequence 2, Application US/09486072  
; Patent No. 6489155  
; GENERAL INFORMATION:  
; APPLICANT: Masanori TAKAYAMA, et al.  
; TITLE OF INVENTION: GENES  
; FILE REFERENCE: 11202/1  
; CURRENT APPLICATION NUMBER: US/09/486,072  
; CURRENT FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: PCT/JF98/02310  
; PRIOR FILING DATE: 1998-05-26  
; PRIOR APPLICATION NUMBER: JP252624/97  
; PRIOR FILING DATE: 1997-09-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 881  
; TYPE: PRT  
; ORGANISM: Bacteria  
US-09-486-072-2

Query Match 6.7%; Score 115.5; DB 4; Length 881;  
Best Local Similarity 22.9%; Pred. No. 0.1;  
Matches 66; Conservative 34; Mismatches 83; Indels 105; Gaps 14;

QY 1 CGGSGSGSSSTPHPKPVLVPTQNNLQAVPQANASQAQANAPQANAPQV 60  
DB 18 CGGSGSEASS-----PEV-----EVDNGVEIQPEPEPEPEPEPEV 56  
QY 61 ENAPQANAPQOVENAPQAEVTPPV-POQ-----SOKIDGSDKIGSVKLNK 106  
DB 57 EPE 110  
QY 107 EAQTELSRFTLVKLTGTPPKFKVSGKKIIEKDFLVNLSD-----INAEQL 155  
DB 111 ESHVNEYQVAPAVEQIAAIP-----GLK-----WLQVNLNGAFGRFIVPVEVEAI 158  
QY 156 SGDFLIRRSDDLFGYHYDNGKLVDA-----DKFSQYFVYVDEKRVNDSKLTATY 211  
DB 159 NPSAPNSADLF-----DPALPGDDLFEQ-----IALGLQAKG 192  
QY 212 RKKEGFVYGSNPHTKFAARISKLGDEIKFENGQAQGSIKDEKDGNA 259  
DB 193 IKVAYIATQGFAMLKGAERS-----MDFDD-----SIVDESDDGA 229

## RESULT 27

US-09-134-001C-5106  
; Sequence 5106, Application US/091344001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Deucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5106  
; LENGTH: 1177  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5106

Query Match 6.7%; Score 115.5; DB 3; Length 1177;  
Best Local Similarity 17.7%; Pred. No. 0.15;  
Matches 68; Conservative 68; Mismatches 161; Indels 87; Gaps 14;

QY 25 QNNLQAVPQANASQAQANAPQANAPQANAPQANAPQANAPQANAPQANAPQAEVTPPV 84  
DB 248 EKNQCKQKQTTAQTSSSENHNVKSNYQTTKRTPNYSKVDNTININIASQIVBEI 307  
QY 85 POPOSQKI--DGSFDKIGSVKLNKEAQTELSRFTLVKLT-----122  
DB 308 RREERKVLQKRFRKALQQRQNNQSQSEDSIOKAIDEMYAKQAQHTGESSLDLENES 367  
QY 123 ---GTPPKFKVSGKKIIEKDFL---VLNLSDINAEQLSGDFLI-----RRSDDL 168  
DB 368 NQDSSNSLEKQSNSSNIDNKEAQNNTPLFNVEIEDLDTTSDVYKVNBEETESKNDEDLV 427  
QY 169 -GYHYDNGKLVDAADKFSQYFVYVDEKVN-----DNISDKLTATYRKKEGFVYGSN 222  
DB 428 SNNHYHSNDAAVEDA-----EYHLDNROQNSQDDIISSKSTSNMYDNAISAV 482  
QY 223 PHTKEFAARISKLGDEIKFENGQAQGSIKDEK-----DGNAEIETI-----K 265  
DB 483 DNTERAKSNEDKNDTEITHLDTTSAKVSDEKIESNTNNHLEODKNVKNVNSLKSN 542  
QY 266 GDTKOLE-----ITPTESNRILITLIDONOKSYT-PCM--EKAIMETKTFIDS 309  
DB 543 SDTGTRKQRFQGGSRPFNVLMTPSDKKK---MMDQNHKKVSPPELKPQANANHRKDS 598  
QY 310 KAGNSDKVLLG---EAKSDNWOA 330  
DB 599 ESNKSEEFKQINTNRETOSNYES 622

## RESULT 28

US-08-613-009A-10  
; Sequence 10, Application US/08613009A  
; Patent No. 6090576  
; GENERAL INFORMATION:  
; APPLICANT: Myers, Lisa E  
; APPLICANT: Schryvers, Anthony B  
; APPLICANT: Harkness, Robin E  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Du, Run-Pan  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/613.009A  
; FILING DATE: 08-MAR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24973  
; REFERENCE/DOCKET NUMBER: 1038-542  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 682 amino acids

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;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-613-009A-10

Query Match
Best Local Similarity 6.6%; Score 114; DB 3; Length 682;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSGSSTPNHFKPVLVPTQNNLQAVPQACNAPQACNAPQACNAPQV 60
Db 1 CG-GSGGS-----NPPAPTPIP-----NAGSGNTGNTAGGTDNTANA 39
QY 61 ENAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQV 120
Db 40 GNTGTSNGTGSANTPEPKY-QDVPTKEKNEK-----DKVSSIQEPAMGYGMAISKINLHN 93
QY 121 KLTGTPPKFQVSGKKIIEKDFVLNLSIDINAEQLSG--DFLIRSDDDLFGYHYDHTNGK 178
Db 94 RQDTP-----LDEKNIIITLGGKKQVAGKKSPLPFLSDVENKLLDGYIAKMN-- 140
QY 179 NLVDAADKFSQYFVVYDE-KRVNDNISDKLTATYRKKEGFVYGSNPHTKPEFAARISKLD 237
Db 141 ----VADKNA-----IGDRIKKNKEISDEBELAKQIKE-----AVRKSHEFQQVLSLEN 186
QY 273 ITPTESNRRIIAILDQNKQSYTFGMBKAINETFKIDSQKAGNSDQKYLIGEAQSDNQWAIM 332
Db 245 ELPTQD-----AVKYKGHDFM--TDVANRRNRFSEVKE--NSQAGWYWGASSKDEYNRL 296
QY 333 VSE 335
Db 297 TKE 299

RESULT 29
US-08-778-570B-12
; Sequence 12, Application US/08778570B
; Patent No. 6437096
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,570B
; FILING DATE: 03-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24973
; REFERENCE/DOCKET NUMBER: 1038-664
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 682 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-778-570B-12

Query Match
Best Local Similarity 6.6%; Score 114; DB 4; Length 682;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSGSSTPNHFKPVLVPTQNNLQAVPQACNAPQACNAPQACNAPQV 60
Db 1 CG-GSGGS-----NPPAPTPIP-----NAGSGNTGNTAGGTDNTANA 39
QY 61 ENAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQACNAPQV 120
Db 40 GNTGTSNGTGSANTPEPKY-QDVPTKEKNEK-----DKVSSIQEPAMGYGMAISKINLHN 93
QY 121 KLTGTPPKFQVSGKKIIEKDFVLNLSIDINAEQLSG--DFLIRSDDDLFGYHYDHTNGK 178
Db 94 RQDTP-----LDEKNIIITLGGKKQVAGKKSPLPFLSDVENKLLDGYIAKMN-- 140
QY 179 NLVDAADKFSQYFVVYDE-KRVNDNISDKLTATYRKKEGFVYGSNPHTKPEFAARISKLD 237
Db 141 ----VADKNA-----IGDRIKKNKEISDEBELAKQIKE-----AVRKSHEFQQVLSLEN 186
QY 273 ITPTESNRRIIAILDQNKQSYTFGMBKAINETFKIDSQKAGNSDQKYLIGEAQSDNQWAIM 332
Db 245 ELPTQD-----AVKYKGHDFM--TDVANRRNRFSEVKE--NSQAGWYWGASSKDEYNRL 296
QY 333 VSE 335
Db 297 TKE 299

RESULT 30
US-09-059-584-12
; Sequence 12, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:
; APPLICANT: Myers, Lisa E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Harkness, Robin E
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,584
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
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STATE: Ontario  
COUNTRY: Canada  
ZIP: MSG IR7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/613,009A  
APPLICATION NUMBER: US/08/613,009A  
FILING DATE: 08-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24973  
REFERENCE/DOCKET NUMBER: 1038-542  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 702 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-613-009A-9

Query Match 6.6%; Score 114; DB 3; Length 702;

Best Local Similarity 21.5%; Pred. No. 0.099;  
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSSSTPNHPKVLVPTKQNNLQAVPQASQAPQAPQAPQAPQV 60  
DB 21 CG--GSGS-----NPPAPTIP-----NASGSGTGTGAGGTDNTANA 59  
QY 61 ENAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQV 120  
DB 60 GNTGSGTSGTANTPEPKY-QDVPTKNEK-----DKVSSIQEPAMGYGMAKSKINLHN 113  
QY 121 KLGTPPKFDKVGSKKIIIEKDFVLNLSLDINAEQLSG--DFLIRSDDLFGYHYHDTNGK 178  
DB 114 RQDTP-----LDEKNIIITLQKQVAGKSKPLPFLSDVENKLLDGYIAKMN-- 160  
QY 179 NLVDAADKFSQYFVWYDE-KRVNDNISDKLTATYRKKEGPFVYGSNPHTKFAARISKGLD 237  
DB 161 ----VADKNA-----IGDKRIKKNKEISDEELAKQIKE-----AVRKSHEFQQVLSLEN 206  
QY 238 VEIKFENGQAGGSIKDEK-----DGNAEIFTIKGD-----TKOLE 272  
DB 207 KIFHSNDGTTKATTRDLKLYDYGYLANDGN--YLTVKTDKLNGLPVGGVFYNGTTTAK 264  
QY 273 IPTESNRRIIAILDQNKSYTPGMEKAIMETKFDISKAGNSDKYLIKEAKSDNQAIM 332  
DB 265 ELPTQD-----AVKYKGHWDFM--TDVANRRNRFSVEKE-NSQAGWYVGASSKDEYNRL 316  
QY 333 VSE 335  
DB 317 TKE 319

RESULT 33  
US-09-074-658-25  
Sequence 25, Application US/09074658  
Patent No. 6184371  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M  
APPLICANT: Run-Pan Du  
APPLICANT: Quijun Wang  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Klein, Michel H  
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: MSG IR7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,658  
FILING DATE: 08-MAY-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-795  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 702 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-074-658-25

Query Match 6.6%; Score 114; DB 3; Length 702;

Best Local Similarity 21.5%; Pred. No. 0.099;  
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CGSGSGSSSTPNHPKVLVPTKQNNLQAVPQASQAPQAPQAPQAPQV 60  
DB 21 CG--GSGS-----NPPAPTIP-----NASGSGTGTGAGGTDNTANA 59  
QY 61 ENAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQAPQV 120  
DB 60 GNTGSGTSGTANTPEPKY-QDVPTKNEK-----DKVSSIQEPAMGYGMAKSKINLHN 113  
QY 121 KLGTPPKFDKVGSKKIIIEKDFVLNLSLDINAEQLSG--DFLIRSDDLFGYHYHDTNGK 178  
DB 114 RQDTP-----LDEKNIIITLQKQVAGKSKPLPFLSDVENKLLDGYIAKMN-- 160  
QY 179 NLVDAADKFSQYFVWYDE-KRVNDNISDKLTATYRKKEGPFVYGSNPHTKFAARISKGLD 237  
DB 161 ----VADKNA-----IGDKRIKKNKEISDEELAKQIKE-----AVRKSHEFQQVLSLEN 206  
QY 238 VEIKFENGQAGGSIKDEK-----DGNAEIFTIKGD-----TKOLE 272  
DB 207 KIFHSNDGTTKATTRDLKLYDYGYLANDGN--YLTVKTDKLNGLPVGGVFYNGTTTAK 264  
QY 273 IPTESNRRIIAILDQNKSYTPGMEKAIMETKFDISKAGNSDKYLIKEAKSDNQAIM 332  
DB 265 ELPTQD-----AVKYKGHWDFM--TDVANRRNRFSVEKE-NSQAGWYVGASSKDEYNRL 316  
QY 333 VSE 335  
DB 317 TKE 319

RESULT 34  
US-08-778-570B-11  
Sequence 11, Application US/08778570B  
Patent No. 6437096  
GENERAL INFORMATION:  
APPLICANT: Wvers, Lisa E  
APPLICANT: Schryvers, Anthony B  
APPLICANT: Harkness, Robin E  
APPLICANT: Loosmore, Sheena M  
APPLICANT: Du, Run-Pan

```

/ APPLICANT: Yang, Yan-Ping
/ APPLICANT: Klein, Michel H
/ TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: 6th Floor, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/778,570B
/ FILING DATE: 03-JAN-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24973
/ REFERENCE/DOCKET NUMBER: 1038-664
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 702 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-778-570B-11

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Query Match 6.6%; Score 114; DB 4; Length 702;
Best Local Similarity 21.5%; Pred. No. 0.099;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CCGSGSGSSSTPNHPKPVLPKTNLQAVPQANASQAQNAPOAQAQNAPOV 60
DB 21 CG--GSGS-----NPPAPTPIP-----NAGSGNTGTGAGGDTNTANA 59

QY 61 ENAPOAQAQNAQVENAQAQAEVTPPQSQKIDGDFKIGSVKLNKEAQTLESRFTLVD 120
DB 60 GNTGTNSTGSGANTPEPKY-QDVTEKNEK-----DKVSSIQEPAMGYGMAKSKINLHN 113

QY 121 KLGTTPPKDKVSGKKIIEKDFVLNLSIDINAQLSG--DFLIRSDDLFGYHYDTNGK 178
DB 114 RQDTP-----LDEKNIITLDGKKQVAEGKKSPLPESLVENKLLDGYIAKMN-- 160

QY 179 NLVDAADKFSQFVYVDE--KRVNDNISDKLTATYRKKEGFVYGSNPHTKFAARISKGLD 237
DB 161 ----VADKNA-----IGDKIKGNKEISDEELAKOIKE-----AVRKSHEFFQVLSLEN 206

QY 238 VEIKFENGQAQGSIKDEK-----DGNAEIITIKGD-----TKOLE 272
DB 207 KIFHSNDGTTKATTRDLKYVDYGYLLANDGN--YLTVKTDLKMLNLPVGVGVYNGITTTAK 264

QY 273 ITPETSNRIIAILDQNKQSYTPGMEKAIMETKFDISKAGNSDKYILIGEAKSDNQAIM 332
DB 265 ELPTQD-----AVKYGHWDPM--TDVANRRNRFSEVKE--NSQAGWYYGASSKDEYNRL 316

QY 333 VSE 335
DB 317 TKE 319

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RESULT 35
US-09-059-584-11
; Sequence 11, Application US/09059584
; Patent No. 6440701
; GENERAL INFORMATION:

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```

/ APPLICANT: Myers, Lisa E
/ APPLICANT: Schryvers, Anthony B
/ APPLICANT: Harkness, Robin E
/ APPLICANT: Loomore, Sheena M.
/ APPLICANT: Du, Run-Pan
/ APPLICANT: Yang, Yan-Ping
/ APPLICANT: Klein, Michel H
/ TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: 6th Floor, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/059,584
/ FILING DATE: 14-APR-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/778,570
/ FILING DATE: 03-JAN-1997
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24973
/ REFERENCE/DOCKET NUMBER: 1038-794
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 702 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-059-584-11

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Query Match 6.6%; Score 114; DB 4; Length 702;
Best Local Similarity 21.5%; Pred. No. 0.099;
Matches 78; Conservative 49; Mismatches 144; Indels 92; Gaps 17;

QY 1 CCGSGSGSSSTPNHPKPVLPKTNLQAVPQANASQAQNAPOAQAQNAPOV 60
DB 21 CG--GSGS-----NPPAPTPIP-----NAGSGNTGTGAGGDTNTANA 59

QY 61 ENAPOAQAQNAQVENAQAQAEVTPPQSQKIDGDFKIGSVKLNKEAQTLESRFTLVD 120
DB 60 GNTGTNSTGSGANTPEPKY-QDVTEKNEK-----DKVSSIQEPAMGYGMAKSKINLHN 113

QY 121 KLGTTPPKDKVSGKKIIEKDFVLNLSIDINAQLSG--DFLIRSDDLFGYHYDTNGK 178
DB 114 RQDTP-----LDEKNIITLDGKKQVAEGKKSPLPESLVENKLLDGYIAKMN-- 160

QY 179 NLVDAADKFSQFVYVDE--KRVNDNISDKLTATYRKKEGFVYGSNPHTKFAARISKGLD 237
DB 161 ----VADKNA-----IGDKIKGNKEISDEELAKOIKE-----AVRKSHEFFQVLSLEN 206

QY 238 VEIKFENGQAQGSIKDEK-----DGNAEIITIKGD-----TKOLE 272
DB 207 KIFHSNDGTTKATTRDLKYVDYGYLLANDGN--YLTVKTDLKMLNLPVGVGVYNGITTTAK 264

QY 273 ITPETSNRIIAILDQNKQSYTPGMEKAIMETKFDISKAGNSDKYILIGEAKSDNQAIM 332
DB 265 ELPTQD-----AVKYGHWDPM--TDVANRRNRFSEVKE--NSQAGWYYGASSKDEYNRL 316

QY 333 VSE 335

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Query Match 6.4%; Score 111.5; DB 2; Length 403;  
Best Local Similarity 21.8%; Pred. No. 0.074;  
Matches 90; Conservative 53; Mismatches 146; Indels 123; Gaps 18;

Qy	4	SGSGSSSTENHEKPLV-----PKTNNLQANVPOAQNASQ-----	41
Db	10	SGPVKATAPVGGPRVLVTQPFCCQPLPVNSGQARVLCPSNSSORVPLQAKLVSSHK	69
Qy	42	-AQNAPQANAPQANAPQVENAP--QAQNAPO-----VENAPQAEVTPPVPOQSQKID	93
Db	70	PVQN--QKQQLQATSVPHVPSRPLNNTQSKQPLPSAPENNPHEELASKQKNEESKKRQ	127
Qy	94	GSFD-----KIGSVKLNKEAQTLELSRFTLVDKLGTTPKPKDKVSGKXIIEEKDF	142
Db	128	WALEDFEIGRPLGKRGFNVYLAREKQ-----SKFIALLKVLFKAQLEKAGVEHQLEREVE	183
Qy	143	LVLNLSIDINAEQLSGDFLIRRSDDLFGYVYHDTGNKLVDAADKFSQYFVYDEKEVNDN	202
Db	184	IQSHLRHPNLLRL-----YGFHDATRVYLI---LEYAPLGTVYRELQKLSK	227
Qy	203	ISDKLTATY-----RKKEGFVYGSNPHTK--EF-----AARI	232
Db	228	FDEQRTATYITELANALSYCHSKRVIHRDIKPENLLIGSAGELKIADFGWSVHAPSSRT	287
Qy	233	SKLGDVEIKFENGQAQGSIXDEK-----DGNAEIFTIKGDTKQLE	272
Db	288	TLCGTLDY-LPPENIEGRMHDEKVDLWSLGLCYEFLVGKPPPEANTYQETK-RISRYE	345
Qy	273	IT-----PTESNRIIIAILDONOKSYTPGMEKAIMETKFI---DSKAGNSDQK	317
Db	346	FTFPDFVTEGARDLISRLKXNPSQRP-MLREVLHPWITANSKSPSCNQNK	396

Search completed: December 17, 2004, 16:02:42  
Job time : 51.7763 secs

(this Page Blank (uspto))

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 15:52:28 ; Search time 203.087 Seconds  
(without alignments)  
595.271 Million cell updates/sec

Title: US-10-696-544-2

Perfect score: 1734

Sequence: 1 CGSGSGGSSSPNHPKPV.....YLIGEAQSDNQAIWVSEKK 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1734	100.0	337	8	Adp82911 rPlpE. 8/
2	221.5	12.8	335	7	Adf29249 Bacterial
3	221.5	12.8	335	7	Adg32458 Pasteurel
4	219	12.6	43	8	Adp82921 Mannheimi
5	186.5	10.8	1164	3	Aay84463 Amino aci
6	178.5	10.3	1135	3	Aay84460 Amino aci
7	177	10.2	984	3	Aay84481 Amino aci
8	177	10.2	1164	2	Aay40537 Group B s
9	177	10.2	1164	3	Aay84459 Amino aci
10	173	10.0	984	2	Aar85782 Group B S
11	173	10.0	1093	2	Aaw40540 Mutant C-
12	173	10.0	1099	2	Aaw40538 Mutant C-
13	173	10.0	1128	2	Aaw40539 Mutant C-
14	173	10.0	1128	3	Aay84461 Amino aci
15	173	10.0	1164	2	Aar85781 Amino aci
16	173	10.0	1164	2	Aaw40541 Mutant C-
17	168	9.7	1129	3	Aay84462 Amino aci
18	165	9.5	1348	2	Aar84665 Outer mem
19	147	8.5	837	4	Abbs8463 Drosophil
20	140.5	8.1	730	2	Aay43385 S. pneumo
21	138.5	8.0	367	2	Aar84666 Outer mem
22	135.5	7.8	1192	4	Abbs8462 Drosophil
23	131	7.6	356	8	Adq30503 Codon-opt
24	131	7.6	478	3	Aab07288 Human IL-
25	129.5	7.5	4365	6	Abu02252 S. pneumo

26	127	7.3	448	8	Adm16778 N. patric
27	127	7.3	485	2	Aaw65462 Neocallim
28	127	7.3	485	2	Aay27283 N. patric
29	127	7.3	485	4	Aab35588 N. patric
30	126	7.3	254	4	Abg16808 Novel hum
31	125.5	7.2	1036	6	Abu36235 Protein e
32	124	7.2	631	2	Aaw08970 Amino aci
33	124	7.2	631	2	Aay51784 H. influe
34	124	7.2	631	2	Aaw54128 H. influe
35	124	7.2	631	3	Aay80366 H. influe
36	124	7.2	917	3	Aay53920 A Bcl-2 a
37	124	7.2	921	7	Ace58793 Human pro
38	124	7.2	930	4	Abg16236 Novel hum
39	123.5	7.1	861	4	Abb59487 Drosophil
40	122	7.0	599	6	Abu35643 Protein e
41	122	7.0	631	2	Aar77896 Bacterial
42	121.5	7.0	3111	4	Abb60327 Drosophil
43	121	7.0	912	8	Adj78291 Marker ge
44	121	7.0	1308	7	Adh88703 Enterococ
45	120.5	6.9	287	7	Adf28364 Adiponect

## ALIGNMENTS

RESULT 1  
ADP82911  
ID ADP82911 standard; protein; 337 AA.  
XX  
AC ADP82911;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE rPlpE.  
XX  
KW recombinant PlpE; Antibacterial; Immunostimulant;  
XX bovine respiratory disease; vaccine.  
XX Mannheimia haemolytica.  
OS  
PN WO2004041182-A2.  
XX  
PD 21-MAY-2004.  
XX  
PF 30-OCT-2003; 2003WO-US034574.  
XX  
PR 30-OCT-2002; 2002US-0422305P.  
XX (OKLA ) UNIV OKLAHOMA STATE.  
PA Confer AW, Ayalew S, Murphy GL, Pandher K;  
XX WPI; 2004-411400/38.  
DR N-PSDB; ADP82910.  
XX  
PT New vaccine compositions comprising a recombinant PlpE outer membrane protein of M. haemolytica optionally in combination with at least one other antigen against M. haemolytica, useful for preventing bovine respiratory disease.  
XX  
PS Example 1; SEQ ID NO 2; 48pp; English.  
XX  
CC The present invention relates to a vaccine composition against infection of M. haemolytica in cattle comprises: recombinant PlpE outer membrane protein of M. haemolytica or its antigenic subunit; or a recombinant PlpE outer membrane protein of M. haemolytica or its antigenic subunits, in combination with at least one other antigen against M. haemolytica; and a pharmaceutical carrier or diluent. The vaccine is useful against infection of M. haemolytica in cattle, or for inducing an immune response in cattle to provide immune protection against bovine respiratory disease and/or shipping fever to an at-risk bovine. The new vaccine provides better protection or immunization than existing commercially available vaccines. The present sequence represents rPlpE.



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30-OCT-2003; 2003WO-US034574.
30-OCT-2002; 2002US-0422305P.
(OKLA ) UNIV OKLAHOMA STATE.
Confer AW, Ayalew S, Murphy GL, Pandher K;
WPI; 2004-411400/38.

New vaccine compositions comprising a recombinant PlpE outer membrane
protein of M. haemolytica optionally in combination with at least one
other antigen against M. haemolytica, useful for preventing bovine
respiratory disease.

Example 2; SEQ ID NO 12; 48bp; English.

The present invention relates to a vaccine composition against infection
of M. haemolytica in cattle comprises: recombinant PlpE outer membrane
protein of M. haemolytica or its antigenic subunit; or a recombinant PlpE
outer membrane protein of M. haemolytica or its antigenic subunits, in a
combination with at least one other antigen against M. haemolytica; and a
pharmaceutical carrier or diluent. The vaccine is useful against
infection of M. haemolytica in cattle, or for inducing an immune response
in cattle to provide immune protection against bovine respiratory disease
and/or shipping fever to an at-risk bovine. The new vaccine provides
better protection or immunization than existing commercially available
vaccines. The present sequence represents Mannheimia haemolytica PlpE
epitope region, out of a total of 8 regions found.

Sequence 43 AA;

Query Match      12.6%; Score 219; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      37 QNASQAQNAPOAQNAPOQNAPOVENAPQNAPOQNAPOVENAPQAE 79
      |||||
DB      1 QNASQAQNAPOAQNAPOQNAPOVENAPQNAPOQNAPOVENAPQAE 43

RESULT 5
AAY84463
ID      AAY84463 standard; protein; 1164 AA.
XX
AC      AAY84463;
XX
DT      25-JUL-2000 (first entry)
DE      Amino acid sequence of a C-beta protein.
XX
KW      C-beta protein; bactericidal; gram positive bacteria; vaccine;
XX      immune response.
XX      Streptococcus agalactiae.
XX      WO200015760-A1.
XX
XX      23-MAR-2000.
XX
XX      17-SEP-1999; 99WO-US021643.
XX
XX      17-SEP-1998; 98US-0100859P.
XX      19-JUL-1999; 99US-0144324P.
XX      15-SEP-1999; 99US-0154017P.
XX
XX      (NAVA-) NORTH AMERICAN VACCINE INC.
XX
XX      Long-Rowe KO, Blake MS;
XX
XX      WPI; 2000-271404/23.
XX      N-PSDB; AAA12456.
XX

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AC AAY84481;  
 XX 25-JUL-2000 (first entry)  
 XX Amino acid sequence of a fragment of the C-beta protein.  
 DE C-beta protein; bactericidal; gram positive bacteria; vaccine;  
 KW immune response.  
 XX Streptococcus agalactiae.  
 OS  
 XX WO200015760-A1.  
 PN 23-MAR-2000.  
 XX 17-SEP-1999; 99WO-US021643.  
 XX 17-SEP-1999; 98US-0100859P.  
 PR 19-JUL-1999; 99US-0144324P.  
 PR 15-SEP-1999; 99US-0154017P.  
 XX (NAVA-) NORTH AMERICAN VACCINE INC.  
 XX Long-Rowe KO, Blake MS;  
 PI WPI; 2000-271404/23.  
 XX Obtaining substantially pure C-beta protein or fragment and/or mutant for  
 PT eliciting antibodies which are bactericidal to gram positive bacteria,  
 PT useful in vaccines.  
 XX Disclosure; Page 153-156; 171pp; English.  
 PS The specification describes a process for obtaining a substantially pure  
 CC C-beta protein. The process comprises obtaining the C-beta protein in  
 CC cell extracts, subjecting the C-beta protein to ion-exchange  
 CC chromatography and collecting the C-beta protein-containing fractions,  
 CC pooling and diluting the fractions, and subjecting the fractions to  
 CC ligand affinity chromatography and collection. The C-beta protein  
 CC fragments are useful for eliciting antibodies which are bactericidal to  
 CC gram positive bacteria with complement alone and therefore is useful in a  
 CC (combination) vaccine together with a pharmaceutically acceptable carrier  
 CC (and/or optionally at least two protein fragments or peptide-  
 CC polysaccharide conjugates). The vaccine therefore is useful in a method  
 CC for inducing an immune response in a mammal. The present sequence  
 CC represents a Streptococcus agalactiae C-beta protein fragment  
 XX Sequence 984 AA;  
 SQ  
 Query Match 10.2%; Score 177; DB 3; Length 984;  
 Best Local Similarity 23.6%; Pred. No. 6e-06;  
 Matches 81; Conservative 44; Mismatches 114; Indels 104; Gaps 15;  
 QY 12 TPNHPKPVLPKTONNLOQNVQQAQNASQAQNAPOAQNAPQVQENAFQANAPQ 71  
 DB 649 TPDPKPIELPQADPTQAPDTPHVPSPKAPAPVPSPKTPPEAFHPVSPKAPAPR 708  
 QY 72 VENAPQAEVTPPVQ---PQSQIDGSDFKIGSVKLNKEAQTLLESLRFTLVDKLGTTPPK 127  
 DB 709 VPSPKTPPEAFHPVSPKTPPEAKLP-----KPKTPDVPKLPDVPKLPDVPK 756  
 QY 128 -----FKVSGK---KIEEK--DFLVNLSDINAEQLSGDFLIRRS 164  
 DB 757 LPDAPKLPDGLNKVGQAVFTSDGNTKTVTVFDRFTDADKLHLKEVTTKELADKIA---- 812  
 QY 165 DDLFVGYHYDNGKLVDAADKFSQYFVVD-----EKRYNDNISDKLTATYRKKEG 216  
 DB 813 -----HKTGGTV-----RVFSLSGKGGKTHVNGERTVRLALQGTGSDV 853  
 QY 217 FVYGSNPHTEFAARISKLGDE---IKFNGQAQGSIKDEKGNARIFITKGTQKLEI 273  
 DB 854 HVY----HVKE-----NGDLERIPSKVENGQV-----FKTNHPSLFAIKULSKDQNV 897

QY 274 TPESNRILAILDQNOKSYTPGMEKAIMET---KFIDSKAGN 313  
 DB 898 TTPKQT-----KPSTQGSQVEIABSOTGKF-QSKAAN 928  
 RESULT 8  
 AAW40537  
 ID AAW40537 standard; protein; 1164 AA.  
 XX AAW40537;  
 XX 17-OCT-2003 (revised)  
 DT 28-AUG-1998 (first entry)  
 XX Group B streptococcal C-beta protein.  
 DE C-beta protein; beta antigen; vaccine; group B Streptococcus.  
 KW Streptococcus sp; strain A909.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide /label= Sig\_peptide  
 FT Protein /label= Mat\_protein  
 FT Region /label= Iga\_binding\_region  
 FT Domain /label= Transmembrane\_domain  
 FT /label= Transmembrane\_domain  
 XX WO9809648-A1.  
 PN 12-MAR-1998.  
 PD 05-SEP-1997; 97WO-US015319.  
 XX 06-SEP-1996; 96US-0024707P.  
 PR (NAVA-) NORTH AMERICAN VACCINE INC.  
 PA Tai JY, Blake MS;  
 PI WPI; 1998-193324/17.  
 XX N-PSDB; AAV11344.  
 DR Group B streptococcal C-beta proteins - having amino acid substitutions to  
 PT reduce immunoglobulin A binding while retaining antigenicity, for use in  
 PT vaccines.  
 XX Claim 1; Fig 1; 59pp; English.  
 PS This polypeptide comprises the wild-type C-beta protein, or beta antigen,  
 CC of a group B Streptococcus that binds to human IGA. The invention relates  
 CC to mutant C-beta proteins (see AAW40538-41) of formula A(X1-X12)B, where  
 CC A comprises amino acids 1-164 of mature C-beta protein, B comprises amino  
 CC acids 177 to 1096-1127 of mature C-beta, and X1-X12 are each selected  
 CC independently from Ala, Val, Leu, Ile, Pro, Met, Phe, Trp, a bond, or the  
 CC corresponding amino acid residue from B-beta protein, provided that at  
 CC least one of X1 to X12 is other than the wild-type amino acid and that  
 CC the LPXTG motif may be missing. Claimed mutant C-beta proteins also have  
 CC hydrophobic amino acid residues 1108-1116 replaced by non-hydrophobic  
 CC amino acid residues, and at least one of amino acid residues 521-541  
 CC (preferably 533-541) either deleted or altered. Vectors comprising  
 CC polynucleotides encoding such proteins, and transformed host cells, are  
 CC claimed. The mutant C-beta proteins have reduced IGA binding while  
 CC retaining most of the antigenicity of the wild-type protein. They can be  
 CC used alone, or conjugated to a polysaccharide, in vaccines for use  
 CC against group B Streptococci (claimed). (Updated on 17-OCT-2003 to  
 CC standardise OS field)  
 XX Sequence 1164 AA;  
 SQ Query Match 10.2%; Score 177; DB 2; Length 1164;

Best Local Similarity	23.6%,	Pred. No.	7.5e-06;
Matches	81;	Conservative	44; Mismatches 114; Indels 104; Gaps 15;
QY	12	TPNHFKPVLPFKTQNNLQAQNVPQAQNAQAPQAQNAQAPQAQNAQAPQAQNAQAPQ	71
Dd	829	TPTDPKPIELPQAADTPQAADTPHVPESPKAPEAPRVESPSTPEAPHVPSPKAPEAPR	888
QY	72	VENAPQAEVTPVQ-----POSOKIDGSDTKGSVKLNKEAQTLSLFTLVDKLTGTPPK	127
Dd	889	VPESFKTPEAPHVPSPKTPEAPKIP-----KPKTPDVPKLPDVPKLPDVPK	936
QY	128	-----FDKVSGK--KIIIEK--DFVLNLSLDINAEQSGDFLRRS	164
Dd	937	LPDAPKLPGLNKGVAVFSTTGNTKTVVPFDPKTADAKLHKVEVTKELADKIA----	992
QY	165	DOLFYGYYHTNGKNLVDAADKFQSFFVVD-----EKKVNDNISDKUTATYRRKEG	216
Dd	993	-----HKTGGGTV-----RVFDLSLGGGKETHVNGERTVRALAQGTGSDV	1033
QY	217	FVYGSNPHTKEFAARISKLDGVE---IKFPENGQAQGSIKDEKGNABETFTIKGTGTLQLEI	273
Dd	1034	HVY----HVKE-----NGDLERISPKVENGVV-----FKTNHFSFLAIKTSKDQNV	1077
QY	274	TPTSNRIIILAILDNQOKSVTPGMEXAIMET---KPIDSAGN	313
Dd	1078	TPPKQT-----KPSIQSQSVEIAAESOTGRF-QSKAAN	1108

RESULT 9	
RAY84459	
ID	RAY84459 standard; protein; 1164 AA.
XX	
AC	RAY84459;
XX	
DT	25-JUL-2000 (first entry)

Obtaining substantially pure C-beta protein or fragment and/or mutant for  
 eliciting antibodies which are bactericidal to gram positive bacteria,  
 useful in vaccines.

Claim 17: Fig 1; 17lpp; English.

The present sequence represents a C-beta protein. The specification  
 describes a process for obtaining a substantially pure C-beta protein.  
 The process comprises obtaining the C-beta protein in cell extracts,  
 subjecting the C-beta protein to ion-exchange chromatography and  
 collecting the C-beta protein-containing fractions, pooling and diluting  
 the fractions, and subjecting the fractions to ligand affinity  
 chromatography and collection. The C-beta protein fragments are useful

CC	for eliciting antibodies which are bactericidal to gram positive bacteria
CC	with complement alone and therefore is useful in a (combination) vaccine
CC	together with a pharmaceutically acceptable carrier (and/or optionally at
CC	least two protein fragments or peptide-polysaccharide conjugates). The
CC	vaccine therefore is useful in a method for inducing an immune response
CC	in a mammal
XX	
XX	
SQ	Sequence 1164 AA;
	Query Match            10.2%; Score 177; DB 3; Length 1164;
	Best Local Similarity 23.6%; Pred. No. 7.5e-06;
Matches	81; Conservative 44; Mismatches 114; Indels 104; Gaps 15;
QY	12 TNNHKPVLVPTKTNMLQNVTPQANASQAQNAPQAQNAPOVNAPQANAPQ 71
DB	: :     : :     : :     : :     : :     : :     : :     : :
DB	829 TDPTTKIPLPQADPTPCADPTHVPESPKAEPSPKTPPEAPHVPESPKAPEAPR 888
QY	72 VENAPQAEVTPVPQ----POSQIKDGSFDKIGSVKLNKEAQTLSRFITLDVKLTGTPK 127
DB	: :
DB	889 VPESKTPPEAPHVPESPKTPEAKLP-----KPPKTPDVFKLPDVFKLPDPVK 936
QY	128 -----FDRVSGK--KIIEBK--DFLVNLMSDINAEQLSGDFLIRRS 164
DB	937 LPDAFKLPGLNKVGQAVFTSTDGNTKVTVFPDKPTDADKLHLKEVTTELADKIA--- 992
QY	165 DDLFGYYHDITNGKLVDAADKFQSQVFVYD-----EKVNDNI SDKLTATYKKEG 216
DB	993 -----HKTGGGV-----RVFDLSLSKGKGKETHVNGERTVRLALGTGSDV 1033
QY	217 FVYGSNPHTEFAARISKLGdVE---IRFENGAQAGSIKDEKXGNAEIFTIKGDTRKOLEI 273
DB	1034 HVI-----HVKE-----NGDLERIPSKVENGVV-----FKTNHFSFLPAIKTSKDQNV 1077
QY	274 TPTESNRILLIDQNQSYTFGEKAIMET---XFIDSKAGN 313
DB	1078 TPpKOT-----KPSTOGSOWEIAESOTGXf-QSKAA 1108

RESULT 10  
AAR85782  
ID AAR85782 standard; protein; 984 AA.  
XX  
AC AAR85782;  
XX  
DT 24-APR-1996 (first entry)  
XX  
XX Group B Streptococcal mutant beta antigen without IgA binding domain.  
DE  
DE Beta antigen; immunoglobulin A; vaccine; streptococci; variant; deletion;  
KW KW immunogen; antibody; probe.  
XX  
XX Streptococcus sp.  
OS  
XX  
XX WO9531478-Al.  
PN  
XX  
XX 23-NOV-1995.  
XX  
XX 15-MAY-1995; 95WO-US006111.  
PF  
XX  
XX 16-MAY-1994; 94US-00242932.  
PR  
XX  
XX (UYFL ) UNIV FLORIDA.  
PA  
XX  
XX Brady L;  
PI  
XX  
XX WPI; 1996-010579/01.  
DR  
XX  
XX Polynucleotide encoding modified group B streptococcal beta antigen -  
PT useful as immunogen in vaccines.  
FT  
XX  
XX Claim 2; Page 29-31; 54pp; English.  
PS  
XX  
XX The beta antigen is a surface expressed protein of Streptococci which is  
CC

CC known to bind to the Fc region of IGA immunoglobulins in a non-immune  
 CC manner. The portion of the beta antigen gene which encodes the IGA  
 CC binding function has been identified and removed to give a truncated beta  
 CC antigen gene whose product (AAW40540) has no IGA binding activity but  
 CC does immunoreact with monospecific anti-beta antigen antisera raised  
 CC against wild-type beta antigen protein. The non-IGA binding form of the  
 CC beta antigen can be used as a component in a human vaccine to protect  
 CC against group B Streptococcal infection  
 CC  
 XX Sequence 984 AA;

Query Match 10.0%; Score 173; DB 2; Length 984;  
 Best Local Similarity 23.3%; Pred. No. 1.3e-05;  
 Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;

QY 12 TPNHPKPVLPKTONNLOQNVPOAQNASQAQNAPOAQNAPQVQENAPQNAPO 71  
 DB 649 TDTPKIPELPOADPTQAPDTPHVPESPKAPEAPRVPSPKTPPEAPHVPSKPAPEAPR 708  
 QY 72 VENAPQAEVTPPVQ-----PQSQKIDGSPDKIGSVKLNKEAQTLELSRFTLVLDKLTGTPPK 127  
 DB 709 VPESPKTPPEAPHVPSPKTPPEAPKIP-----EPPKTPDVPKLPDVPKLPDVPK 756  
 QY 128 -----FDKVGSK---KIIEEK--DFLVNLSDINAEQLSGDFLIRRS 164  
 DB 757 LPDAPKLPDGLNKGQAVFTSTDGNTKVTWVDFDKPTDADKLHLKEVTTKELADKIA---- 812  
 QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVYD-----EKRVDNISDKLTATYRKKEG 216  
 DB 813 -----HKTGGTV-----RVFDLSLKGKETHVNGERTVRLALGQTGSDV 853  
 QY 217 FVYGSNPHTKFAARISKLGDEVE---IKFENGQAQGSIKDEKGNABEFTIKGDTKQLEI 273  
 DB 854 HVY-----HVKE-----NGDLERIPSKVENGQV-----FKTNHFSLFAIKTILSKQNV 897  
 QY 274 TPTESNRIIAILDQNKSVTPGMEKAIMET---KFDISKAGN 313  
 DB 898 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 928

RESULT 11  
 AAW40540  
 ID AAW40540 standard; protein; 1093 AA.  
 XX AC AAW40540;  
 XX DT 28-AUG-1998 (first entry)  
 XX DE Mutant C-beta protein dgb1.  
 XX XX C-beta protein; beta antigen; vaccine; group B Streptococcus.  
 XX OS Streptococcus sp; strain A909.  
 XX OS Synthetic.  
 XX PN WO9809648-A1.  
 XX PD 12-MAR-1998.  
 XX PF 05-SEP-1997; 97WO-US015319.  
 XX PR 06-SEP-1996; 96US-0024707P.  
 XX PA (NAVA-) NORTH AMERICAN VACCINE INC.  
 XX PI Tai JY, Blake MS;  
 XX PT WPI; 1998-193324/17.  
 XX DR N-PSDB; AAV11347.  
 XX XX Group B streptococcal Cbeta proteins - having amino acid substitutions to  
 PT reduce immunoglobulin A binding while retaining antigenicity, for use in  
 PT vaccines.

XX Disclosure; Fig 8A-C; 59pp; English.  
 XX CC Group B Streptococcus C-beta mutant protein dgb1 has 0% of the IGA  
 CC binding activity of the native C-beta protein (see AAW40537). It is  
 CC encoded by mutated C-beta protein DNA (see AAV11347) in which codons 168-  
 CC 175 are deleted and replaced by a codon for Glu and a codon for Ala.  
 CC These residues are in the IGA binding domain of the C-beta protein. The  
 CC IGA binding ability of C-beta appears to require dimerisation of the  
 CC protein. The invention relates to mutant C-beta proteins that have a  
 CC reduced or eliminated ability to bind human IGA but which retain the  
 CC antigenicity of the wild-type protein. Such proteins can be used in  
 CC vaccines for use against group B streptococci. Claimed mutant proteins  
 CC have mutations in the IGA binding region of C-beta  
 XX  
 XX Sequence 1093 AA;

Query Match 10.0%; Score 173; DB 2; Length 1093;  
 Best Local Similarity 23.3%; Pred. No. 1.5e-05;  
 Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;

QY 12 TPNHPKPVLPKTONNLOQNVPOAQNASQAQNAPOAQNAPQVQENAPQNAPO 71  
 DB 787 TDTPKIPELPOADPTQAPDTPHVPESPKAPEAPRVPSPKTPPEAPHVPSKPAPEAPR 846  
 QY 72 VENAPQAEVTPPVQ-----PQSQKIDGSPDKIGSVKLNKEAQTLELSRFTLVLDKLTGTPPK 127  
 DB 847 VPESPKTPPEAPHVPSPKTPPEAPKIP-----EPPKTPDVPKLPDVPKLPDVPK 894  
 QY 128 -----FDKVGSK---KIIEEK--DFLVNLSDINAEQLSGDFLIRRS 164  
 DB 895 LPDAPKLPDGLNKGQAVFTSTDGNTKVTWVDFDKPTDADKLHLKEVTTKELADKIA---- 950  
 QY 165 DDLFYGYHDTNGKLVDAADKFSQYFVVYD-----EKRVDNISDKLTATYRKKEG 216  
 DB 951 -----HKTGGTV-----RVFDLSLKGKETHVNGERTVRLALGQTGSDV 991  
 QY 217 FVYGSNPHTKFAARISKLGDEVE---IKFENGQAQGSIKDEKGNABEFTIKGDTKQLEI 273  
 DB 992 HVY-----HVKE-----NGDLERIPSKVENGQV-----FKTNHFSLFAIKTILSKQNV 1035  
 QY 274 TPTESNRIIAILDQNKSVTPGMEKAIMET---KFDISKAGN 313  
 DB 1036 TPKQT-----KPTQGSQVEIAESQTGKF-QSKAAN 1066

RESULT 12  
 AAW40538  
 ID AAW40538 standard; protein; 1099 AA.  
 XX AC AAW40538;  
 XX DT 28-AUG-1998 (first entry)  
 XX DE Mutant C-beta protein dgb2.  
 XX XX C-beta protein; beta antigen; vaccine; group B Streptococcus.  
 XX OS Streptococcus sp; strain A909.  
 XX OS Synthetic.  
 XX PN WO9809648-A1.  
 XX PD 12-MAR-1998.  
 XX PF 05-SEP-1997; 97WO-US015319.  
 XX PR 06-SEP-1996; 96US-0024707P.  
 XX PA (NAVA-) NORTH AMERICAN VACCINE INC.  
 XX PI Tai JY, Blake MS;  
 XX XX



XX 30-APR-1996 (first entry)  
XX Group B Streptococcal wild-type beta antigen.  
XX Beta antigen; immunoglobulin A; vaccine; streptococci; variant; deletion;  
XX immunogen; antibody; probe.  
XX Streptococcus sp.  
XX Key Location/Qualifiers  
XX Peptide 1. 37  
XX Peptide /label= sig\_peptide  
XX Peptide 38. 1164  
XX Peptide /label= mat\_peptide  
XX WO9531478-A1.  
XX 23-NOV-1995.  
XX 15-MAY-1995; 95WO-US006111.  
XX 16-MAY-1994; 94US-00242932.  
XX (UVFL ) UNIV FLORIDA.  
XX Brady L;  
XX WPI; 1996-010879/01.  
XX N-PSDB; AAT03190.  
XX Polynucleotide encoding modified group B streptococcal beta antigen -  
XX useful as immunogen in vaccines.  
XX Disclosure; Page 29-31; 54pp; English.  
XX AAR85781 is the wild-type group B Streptococcal beta antigen. The beta  
XX antigen is a surface expressed protein of Streptococci which is known to  
XX bind to the Fc region of IgA immunoglobulins in a non-immune manner. The  
XX portion of the beta antigen gene which encodes the IgA binding function  
XX has been identified and removed to give a truncated beta antigen gene  
XX whose product (AAR85782) has no IgA binding activity but does immunoreact  
XX with monospecific anti-beta antigen antisera raised against wild-type  
XX beta antigen protein. The non-IgA binding form of the beta antigen can be  
XX used as a component in a human vaccine to protect against group B  
XX Streptococcal infection  
XX Sequence 1164 AA;  
Query Match 10.0%; Score 173; DB 2; Length 1164;  
Best Local Similarity 23.3%; Pred. No. 1.7e-05;  
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;  
QY 12 TPNHKPVLPVKTQNNLQAVPQQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71  
Db 829 TPTDKIPQLPQAPDTPQAPDTPHVPSPKAPAPRVPSPKTPEAPHVPSKAPAPR 888  
QY 72 VENAPQAEVTPVPQ-----PQSQKIDGSDFKIGSVKLNKEAQTLELSRFTLVKLTGTPPK 127  
Db 889 VPESPKTPEAPHVPSKTPPEAKIP-----EPKTPDVPKLPDVPKLPDVPK 936  
QY 128 -----FDKVGSK---KIIIEK---DFLVNLSINAQQLSGDFLIIRS 164  
Db 937 LPDAPKLPDGLNKVGQAVFTSDGNTKTVTVFDPKPTDADKHLKEVTTKELADKIA---- 992  
QY 165 DDLFYGYHDTNGKNLVDAADKFSQYFVYD-----EKVNDNISDKLTATYRKKEG 216  
Db 993 -----HKTGGTV-----RVFDLSLSKGGKETHVNGERTVRLALGQTGSDV 1033  
QY 217 FVYGSNPHTEFAARISKIGDVE---IKFENGQAQGSIKDEKDGNAEIFTIKGDTKQLEI 273  
Db 1034 HVI-----HVKE-----NGDLERIPSKVNGQV-----FKTNHSLFAIKLTSDQNV 1077  
QY 274 TPTESNRIIAILDQNKQSYTPGMEKAIMET---KPIDSKAGN 313

DT 30-APR-1996 (first entry)  
XX Group B Streptococcal wild-type beta antigen.  
XX Beta antigen; immunoglobulin A; vaccine; streptococci; variant; deletion;  
XX immunogen; antibody; probe.  
XX Streptococcus sp.  
XX Key Location/Qualifiers  
XX Peptide 1. 37  
XX Peptide /label= sig\_peptide  
XX Peptide 38. 1164  
XX Peptide /label= mat\_peptide  
XX WO9531478-A1.  
XX 23-NOV-1995.  
XX 15-MAY-1995; 95WO-US006111.  
XX 16-MAY-1994; 94US-00242932.  
XX (UVFL ) UNIV FLORIDA.  
XX Brady L;  
XX WPI; 1996-010879/01.  
XX N-PSDB; AAT03190.  
XX Polynucleotide encoding modified group B streptococcal beta antigen -  
XX useful as immunogen in vaccines.  
XX Disclosure; Page 29-31; 54pp; English.  
XX AAR85781 is the wild-type group B Streptococcal beta antigen. The beta  
XX antigen is a surface expressed protein of Streptococci which is known to  
XX bind to the Fc region of IgA immunoglobulins in a non-immune manner. The  
XX portion of the beta antigen gene which encodes the IgA binding function  
XX has been identified and removed to give a truncated beta antigen gene  
XX whose product (AAR85782) has no IgA binding activity but does immunoreact  
XX with monospecific anti-beta antigen antisera raised against wild-type  
XX beta antigen protein. The non-IgA binding form of the beta antigen can be  
XX used as a component in a human vaccine to protect against group B  
XX Streptococcal infection  
XX Sequence 1164 AA;  
Query Match 10.0%; Score 173; DB 2; Length 1164;  
Best Local Similarity 23.3%; Pred. No. 1.7e-05;  
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;  
QY 12 TPNHKPVLPVKTQNNLQAVPQQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71  
Db 829 TPTDKIPQLPQAPDTPQAPDTPHVPSPKAPAPRVPSPKTPEAPHVPSKAPAPR 888  
QY 72 VENAPQAEVTPVPQ-----PQSQKIDGSDFKIGSVKLNKEAQTLELSRFTLVKLTGTPPK 127  
Db 889 VPESPKTPEAPHVPSKTPPEAKIP-----EPKTPDVPKLPDVPKLPDVPK 936  
QY 128 -----FDKVGSK---KIIIEK---DFLVNLSINAQQLSGDFLIIRS 164  
Db 937 LPDAPKLPDGLNKVGQAVFTSDGNTKTVTVFDPKPTDADKHLKEVTTKELADKIA---- 992  
QY 165 DDLFYGYHDTNGKNLVDAADKFSQYFVYD-----EKVNDNISDKLTATYRKKEG 216  
Db 993 -----HKTGGTV-----RVFDLSLSKGGKETHVNGERTVRLALGQTGSDV 1033  
QY 217 FVYGSNPHTEFAARISKIGDVE---IKFENGQAQGSIKDEKDGNAEIFTIKGDTKQLEI 273  
Db 1034 HVI-----HVKE-----NGDLERIPSKVNGQV-----FKTNHSLFAIKLTSDQNV 1077  
QY 274 TPTESNRIIAILDQNKQSYTPGMEKAIMET---KPIDSKAGN 313

XX 23-MAR-2000.  
XX 17-SEP-1999; 99WO-US021643.  
XX 17-SEP-1998; 98US-0100859P.  
XX 19-JUL-1999; 99US-0144324P.  
XX 15-SEP-1999; 99US-0154017P.  
XX (NAVA-) NORTH AMERICAN VACCINE INC.  
XX PA Long-Rowe KO, Blake MS;  
XX PI WPI; 2000-271404/23.  
XX DR N-PSDB; AAA12454.  
XX Obtaining substantially pure C-beta protein or fragment and/or mutant for  
XX eliciting antibodies which are bactericidal to gram positive bacteria,  
XX useful in vaccines.  
XX Disclosure; Page 121-125; 171pp; English.  
XX The specification describes a process for obtaining a substantially pure  
XX C-beta protein. The process comprises obtaining the C-beta protein in  
XX cell extracts, subjecting the C-beta protein to ion-exchange  
XX chromatography and collecting the C-beta protein-containing fractions,  
XX pooling and diluting the fractions, and subjecting the fractions to  
XX ligand affinity chromatography and collection. The C-beta protein  
XX fragments are useful for eliciting antibodies which are bactericidal to  
XX gram positive bacteria with complement alone and therefore is useful in a  
XX (combination) vaccine together with a pharmaceutically acceptable carrier  
XX (and/or optionally at least two protein fragments or peptide-  
XX polysaccharide conjugates). The vaccine therefore is useful in a method  
XX for inducing an immune response in a mammal. The present sequence  
XX represents a Streptococcus agalactiae C-beta protein  
XX Sequence 1128 AA;  
Query Match 10.0%; Score 173; DB 3; Length 1128;  
Best Local Similarity 23.3%; Pred. No. 1.6e-05;  
Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;  
QY 12 TPNHKPVLPVKTQNNLQAVPQQAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQNAQ 71  
Db 793 TPTDKIPQLPQAPDTPQAPDTPHVPSPKAPAPRVPSPKTPEAPHVPSKAPAPR 852  
QY 72 VENAPQAEVTPVPQ-----PQSQKIDGSDFKIGSVKLNKEAQTLELSRFTLVKLTGTPPK 127  
Db 853 VPESPKTPEAPHVPSKTPPEAKIP-----EPKTPDVPKLPDVPKLPDVPK 900  
QY 128 -----FDKVGSK---KIIIEK---DFLVNLSINAQQLSGDFLIIRS 164  
Db 901 LPDAPKLPDGLNKVGQAVFTSDGNTKTVTVFDPKPTDADKHLKEVTTKELADKIA---- 956  
QY 165 DDLFYGYHDTNGKNLVDAADKFSQYFVYD-----EKVNDNISDKLTATYRKKEG 216  
Db 957 -----HKTGGTV-----RVFDLSLSKGGKETHVNGERTVRLALGQTGSDV 997  
QY 217 FVYGSNPHTEFAARISKIGDVE---IKFENGQAQGSIKDEKDGNAEIFTIKGDTKQLEI 273  
Db 998 HVI-----HVKE-----NGDLERIPSKVNGQV-----FKTNHSLFAIKLTSDQNV 1041  
QY 274 TPTESNRIIAILDQNKQSYTPGMEKAIMET---KPIDSKAGN 313  
Db 1042 TPKQT-----KPSQGSQVEIABSQTGKF-QSKAAN 1072  
RESULT 15  
AAR85781  
ID AAR85781 standard; protein; 1164 AA.  
XX AAR85781;  
XX

Db 1078 TTPKQT-----KPTSGSQVEIAESQTGKF-QSKAAN 1108  
 RESULT 16  
 ID AAW40541 standard; protein; 1164 AA.  
 AC AAW40541;  
 XX  
 DT 28-AUG-1998 (first entry)  
 XX  
 DE Mutant C-beta protein pnv231.  
 XX  
 KW C-beta protein; beta antigen; vaccine; group B Streptococcus.  
 OS Streptococcus sp; strain A909.  
 OS Synthetic.  
 XX  
 PN WO9809648-A1.  
 XX  
 PD 12-MAR-1998.  
 XX  
 PF 05-SEP-1997; 97WO-US015319.  
 XX  
 PR 06-SEP-1996; 96US-0024707P.  
 XX  
 PA (NAVA-) NORTH AMERICAN VACCINE INC.  
 XX  
 PI Tai JY, Blake MS;  
 XX  
 DR WPI; 1998-193324/17.  
 DR N-PSDB; AAV11348.  
 XX  
 Group B streptococcal Cbeta proteins - having amino acid substitutions to  
 PT reduce immunoglobulin A binding while retaining antigenicity, for use in  
 PT vaccines.  
 XX  
 PS Disclosure; Fig 9A-C; 59pp; English.  
 XX  
 CC Group B Streptococcus C-beta mutant protein pnv231 has only 60% of the  
 CC IGA binding activity of the native C-beta protein (see AAW40537). It is  
 CC encoded by mutated C-beta protein DNA (see AAV11348) in which the Lys-170  
 CC and Lys-175 codons of the mature C-beta protein coding region are  
 CC respectively replaced by a Thr codon and by a Leu codon. These residues  
 CC are in the IGA binding domain of the C-beta protein. The IGA binding  
 CC ability of C-beta appears to require dimerisation of the protein. The  
 CC invention relates to mutant C-beta proteins that have a reduced or  
 CC eliminated ability to bind human IGA but which retain the antigenicity of  
 CC the wild-type protein. Such proteins can be used in vaccines for use  
 CC against group B streptococci. Claimed mutant proteins have mutations in  
 CC the IGA binding region of C-beta  
 XX  
 SQ Sequence 1164 AA;  
 Query Match 10.0%; Score 173; DB 2; Length 1164;  
 Best Local Similarity 23.3%; Pred. No. 1.7e-05;  
 Matches 80; Conservative 45; Mismatches 114; Indels 104; Gaps 15;  
 QY 12 TPNHPKVLVPKTNQNI-QAQNVPQAQNASQAQNAPOAQNAPQVNAPOAQNAPQ 71  
 Db 829 TPDTPKIPFLPQAPDTPQAPDTPHPSPKAPAPRVPSPKTPPEAPHVPSKAPAPR 888  
 QY 72 VENAPQAEVTPVPVQ----PQSQKIDGSPDKIGSVKLNKEAQTLSESRFLVDKLTGTPK 127  
 Db 889 VPESPKTPPEAPHVPSKTPPEAKIP-----EPKTPDVPKLPDVPKLPDVPK 936  
 QY 128 -----FDKVSQK---KIIEBK--DFLVNLSIDNAEQLSGDFLIRRS 164  
 Db 937 LPDAPKLPDGLNKVQAVFTSDGNTKVTVVFDKPTDADKLHLKEVTTRELADKIA--- 992  
 QY 165 DDLFYGYHDTNGKLVDAADKFSQFVVVD-----EKRYNDNISKLTATYRKKG 216

Db 993 -----HKTGGTV-----RVFDLSLSKGGKETHVNGERTVRLALGOTGSDV 1033  
 QY 217 FVYGSNPHTKFAARISKLGVE----IKFENQQAQGSINDEKQNAEIFTIKGDTKQLEI 273  
 Db 1034 HVY-----HVKE-----NGDLERIPSKVENGQVV-----FKTNHFSLFAIKTLSDQNV 1077  
 QY 274 TPTESNRIIAILDQNKSYTPTGMEKAIMET---KFIDSKAGN 313  
 Db 1078 TTPKQT-----KPTSGSQVEIAESQTGKF-QSKAAN 1108  
 RESULT 17  
 ID AAY84462 standard; protein; 1129 AA.  
 AC AAY84462;  
 XX  
 DT 25-JUL-2000 (first entry)  
 XX  
 DE Amino acid sequence of a C-beta protein.  
 XX  
 KW C-beta protein; bactericidal; gram positive bacteria; vaccine;  
 KW immune response.  
 XX  
 OS Streptococcus agalactiae.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 19 /note= "encoded by TAA"  
 FT Misc-difference 23 /note= "encoded by TAA"  
 FT Misc-difference 31 /note= "encoded by TAA"  
 FT  
 XX WO200015760-A1.  
 XX  
 PD 23-MAR-2000.  
 XX  
 PF 17-SEP-1999; 99WO-US021643.  
 XX  
 PR 17-SEP-1998; 98US-0100859P.  
 PR 19-JUL-1999; 99US-0144324P.  
 PR 15-SEP-1999; 99US-0154017P.  
 XX  
 PA (NAVA-) NORTH AMERICAN VACCINE INC.  
 XX  
 PI Long-Rowe KO, Blake MS;  
 DR WPI; 2000-271404/23.  
 DR N-PSDB; AAA12455.  
 XX  
 PT Obtaining substantially pure C-beta protein or fragment and/or mutant for  
 PT eliciting antibodies which are bactericidal to gram positive bacteria,  
 PT useful in vaccines.  
 XX  
 PS Disclosure; page 131-134; 171pp; English.  
 XX  
 CC The specification describes a process for obtaining a substantially pure  
 CC C-beta protein. The process comprises obtaining the C-beta protein in  
 CC cell extracts, subjecting the C-beta protein to ion-exchange  
 CC chromatography and collecting the C-beta protein-containing fractions,  
 CC pooling and diluting the fractions, and subjecting the fractions to  
 CC ligand affinity chromatography and collection. The C-beta protein  
 CC fragments are useful for eliciting antibodies which are bactericidal to  
 CC gram positive bacteria with complement alone and therefore is useful in a  
 CC (combination) vaccine together with a pharmaceutically acceptable carrier  
 CC (and/or optionally at least two protein fragments or peptide-  
 CC polysaccharide conjugates). The vaccine therefore is useful in a method  
 CC for inducing an immune response in a mammal. The present sequence  
 CC represents a Streptococcus agalactiae C-beta protein  
 XX  
 SQ Sequence 1129 AA;

[illegible]

RESULT 19  
ABBS8463  
ID ABB58463 standard; protein; 837 AA.  
XX  
XX AC ABB58463;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
XX Drosophila melanogaster polypeptide SEQ ID NO 2181.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
XX Drosophila melanogaster.  
XX  
XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US009231.  
XX  
XX 23-MAR-2000; 2000US-0191637P.  
XX 11-JUL-2000; 2000US-00614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI; 2001-656860/75.  
XX DR N-PSDB; ABL02566.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX  
XX Disclosure; SEQ ID NO 2181; 21pp + Sequence Listing; English.  
PS  
XX

CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 837 AA;  
 SQ

Query Match 8.5%; Score 147; DB 4; Length 837;  
 Best Local Similarity 24.4%; Pred. No. 0.0018;  
 Matches 77; Conservative 52; Mismatches 126; Indels 60; Gaps 14;  
 17 KPVLVPTQNNLQONVPOQAQNASQAQNAPOQAQNAPOQVFNAPQNAPOVE--- 73  
 474 KPVL--KKQDAQKKQ--FKPLKERSNKKTKMLNEKETTDKQTKKXKXTENSPVVEIS 530  
 74 NAOQAEVTPVPPOQOSKIDGSP--DKIGSVKLKNEAQTLELSRFTLVKLGTPPKFDKV 131  
 531 SDPDVEIKPEVKETNREGDAHETETNEVERDREEQFVD-----ATEKNTDEA 580  
 132 SGKIIIEKDFLVNLSINAEQLSGDPLIRSDDLFGVYHDTNGKNLVDAADKFSQYF 191  
 581 KEKKV--KDPPELKEAD--NSEEKSD---AREEVLL-----DEDEKNLEENAAEISDNA 629  
 192 VYDEKRVNDNISDKLTATYRKSGFVYGSNPHTKFAARISKLDGVEIKFENGQAQCSI 251  
 630 VKSLEKPTNEDRVEK-----VEDEVEHAEEFS-----DLPTP---PQLPSTT 668  
 252 KDEKGNAEIETIKGDTKQL-----ETPTESNRILIIILDQNKSYTFGME-----KAI 301  
 669 DDNEDDVLEIQTSLDDVQLHTPSRQSTPKSRRLSDSGSDCSFKSASDNAKLACQAI 728  
 302 METKFDISKAGNSDQ 316  
 729 EETEOKASKAFNDDE 743

RESULT 20  
 AAY43385  
 ID AAY43385 standard; protein; 730 AA.  
 XX  
 AC AAY43385;  
 XX  
 DT 27-JAN-2000 (first entry)  
 XX  
 DE S. pneumoniae PspC protein sequence.  
 XX  
 KW PspC gene; pneumococcal surface protein C; epitope; diagnosis;  
 KW epitopic region; immunogenic composition; vaccine composition; therapy;  
 KW meningitis; immunological response; otitis media; bacteraemia; pneumonia;  
 KW anti-PspA antibody.  
 XX  
 OS Streptococcus pneumoniae.  
 XX  
 PN WO9953940-A1.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 23-APR-1999; 99WO-US008895.  
 XX  
 PR 23-APR-1999; 99US-0082728P.  
 XX  
 PA (UYAL-) UNIV ALABAMA.  
 XX  
 PI Briles DE, Hollingshead SK, Brooks-Walter A;  
 XX  
 DR WPI; 1999-620581/53.  
 DR N-PSDB; AAZ31957.

XX New epitope polypeptides of *Pneumococcal* surface protein C, used to  
 PT develop products for immunological, immunogenic or vaccine compositions,  
 PT particularly against *Streptococcus pneumoniae* infections.  
 XX  
 XX Example; Fig 15; 109pp; English.  
 XX  
 CC This sequence is the *Streptococcus pneumoniae* pneumococcal surface  
 CC protein C. The invention relates to an isolated and/or purified  
 CC polypeptide comprising at least one epitope or epitopic region of  
 CC *Pneumococcal* surface protein C (PspC). The polypeptides or vectors  
 CC containing sequence encoding them can be used as immunogenic,  
 CC immunological or vaccine compositions. The compositions can be used for  
 CC eliciting an immunological response against *Streptococcus pneumoniae*  
 CC (SP), which can cause otitis media, meningitis, bacteraemia and  
 CC pneumonia. They can be used for eliciting an anti-PspA antibody. The  
 CC nucleic acid molecules can also be used for detecting pspC, pspA or SP  
 XX  
 XX Sequence 730 AA;  
 SQ

Query Match 8.1%; Score 140.5; DB 2; Length 730;  
 Best Local Similarity 35.8%; Pred. No. 0.0055;  
 Matches 29; Conservative 16; Mismatches 35; Indels 1; Gaps 1;  
 13 PNHKPKVLVPTQNNLQONVPOQAQNASQAQNAPOQAQNAPOQVFNAPQNAPOV 72  
 594 PEAPKSPVVKYKPEAPKAPDTPQVPEAPKSPVVKVSDTPKAPDTPQVPEAPKSPV 653  
 73 ENAPOAEVTPVPQ--PQSQKI 92  
 654 PEAPKAPDTPQVPEAPKSPV 674

RESULT 21  
 AAR54666  
 ID AAR54666 standard; protein; 367 AA.  
 XX  
 AC AAR54666;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 06-NOV-1994 (first entry)  
 XX  
 DE Outer membrane lipoprotein A.  
 XX  
 KW OMP; *Actinobacillus pleuropneumoniae*; AP; vaccine; pigs; probe.  
 XX  
 OS *Actinobacillus pleuropneumoniae*.  
 XX  
 PN WO9410316-A1.  
 XX  
 PD 11-MAY-1994.  
 XX  
 PF 03-NOV-1993; 93WO-CA000448.  
 XX  
 PR 05-NOV-1992; 92US-00971558.  
 XX  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 XX  
 PI Gerlach GF, Willison PJ, Rossi-Campos A, Potter AA;  
 XX  
 DR WPI; 1994-167471/20.  
 DR N-PSDB; AAQ65354.  
 XX  
 PT Pure *actinobacillus pleuropneumoniae* outer membrane lipoprotein - used in  
 PT vaccines for treating or preventing infection, partic. in pigs and for  
 PT diagnosis.  
 XX  
 PS Claim 1; Fig 2; 59pp; English.  
 XX  
 CC *Actinobacillus pleuropneumoniae* was cultured and outer membrane protein  
 CC (OMPs) were isolated and analysed. AP culture supernatant was used to  
 CC raise rabbit antiserum which was used to screen an AP strain AP 213  
 CC genomic DNA library in *E. coli* to obtain DNA encoding AP serotype 5 OmlA.







XX Claim 1; SEQ ID NO 3660; 56pp; English.

PS The invention relates to a protein comprising or having at least 50%

XX identity to any of the 2469 amino acid sequences, identified in the

CC specification (available on a computer readable format), or its fragment,

CC expressed from 2469 of 2489 identified DNA coding regions from the

CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as

CC AS55454. Also included are an antibody which binds one of the proteins,

CC treating a patient by administering the protein, DNA or antibody (in a

CC composition), a kit comprising first and second primers, which are the

CC nucleic acid cited above or fragments between nucleotides 8-100 of a

CC sequence not defined in the specification, for amplifying a target

CC sequence contained within a Streptococcus nucleic acid sequence, where

CC the first primer is substantially complementary to the target sequence

CC and the second primer is substantially complementary to the complement of

CC the target sequence, and where the parts of the primers having

CC substantial complementarity define the termini of the target sequence to

CC be amplified, assay comprising contacting a test compound with the

CC protein, and determining whether the test compound binds to the protein

CC and a Streptococcus pneumoniae bacterium, where one or more genes

CC encoding the proteins has been rendered inactive. The proteins, nucleic

CC acid molecules, antibody and compositions are useful as medicaments for

CC treating or preventing a disease or infection due to streptococcus

CC bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis

CC media or ear infection. They are also useful in developing vaccines,

CC diagnostics and antibiotics. The methods are useful for identifying

CC immunodominant proteins. The present sequence is one of the 2469 proteins

CC expressed by the identified coding regions from the genomic sequence.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 23-OCT-2003 to

CC standardise OS field)

XX Sequence 4365 AA;

XX Query Match 7.5%; Score 129.5; DB 6; Length 4365;

XX Best Local Similarity 38.1%; Pred. No. 0.57; 23; Indels 29; Gaps 4;

XX Matches 37; Conservative 8; Mismatches 29; Gaps 4;

QY 18 PVLVPTQNNLQAGN--VPOAQNASQAQN-----APQAQNAPOAQ 55

DB 36 PVLOSQHQVLPQHRQVRLQQAQHLNQRPVLRLLQVPLQLQHQPAPRPQAPQLL 95

QY 56 NAOVENAQAQNAPOAQAQVETPPVPPQSQKI 92

DB 96 NRPO--PAPRPQAPQLLRPQ-----PAPQPQHQRV 125

RESULT 26

ADM16778

XX ADM16778 standard; protein; 448 AA.

XX AC ADM16778;

XX DT 03-JUN-2004 (first entry)

XX DE N. patriciarum xylanase #1.

XX KW xylanase; food; feed; pulp industry; paper industry; enzyme.

XX OS Neocallimastix patriciarum.

XX FN US2004053238-A1.

XX PD 18-MAR-2004.

XX PF 17-SEP-2002; 2002US-00244596.

XX PR 17-SEP-2002; 2002US-00244596.

XX (HSEU/) HSEU R.

XX (HUAN/) HUANG Y.

XX Hseu R, Huang Y;

XX WPI; 2004-327305/30.

DR New recombinant thermo- and alkaline pH-tolerable xylanases derived from

XX anaerobic fungi, useful in a number of applications e.g. in the food,

PT feed, and particularly in the pulp and paper industries.

XX Example 4; SEQ ID NO 14; 48pp; English.

XX The invention relates to a xylanase or its xylanolytic fragments. The

CC methods and compositions of the present invention are useful in a number

CC of applications in the food, feed, and particularly in the pulp and paper

CC industries. The present sequence represents the amino acid sequence of a

CC N. patriciarum xylanase.

XX Sequence 448 AA;

XX Query Match 7.3%; Score 127; DB 8; Length 448;

XX Best Local Similarity 36.8%; Pred. No. 0.041;

XX Matches 35; Conservative 10; Mismatches 44; Indels 6; Gaps 4;

QY 2 GSGSGSGSSPTNPKPVLVPTQNNLQAGNVPOAQNASQAQNAPOAQAQNAPOVE 61

DB 240 GGAPAGGAPAGNDPQG---PQGQPPQGGPPQGGPPQGGPPQGG-NDQGGQ 295

QY 62 NAOQAQNAPOAQAQVETPPVPO--POSQKIDGS 95

DB 296 QPPQGGPPQGGNDQGGQ--QPPQGGPPQGGNPGGS 329

RESULT 27

AAW65462

XX AAW65462 standard; protein; 485 AA.

XX AC AAW65462;

XX DT 17-OCT-2003 (revised)

XX DT 09-NOV-1998 (first entry)

XX DE Neocallimastix patriciarum endo-xylanase.

XX KW Endo-xylanase; xynC gene; transgenic plant; Brassica napus; oilseed rape;

XX canola; feedstuff.

XX OS Neocallimastix patriciarum; strain 27.

XX FH Key Location/Qualifiers

XX FT Peptide 1..20

XX FT /label= Sig peptide

XX FT /note= "putative signal peptide"

XX FT 21..485

XX FT /label= Mat\_protein

XX CA2190194-A.

XX PN 13-MAY-1998.

XX PD 13-NOV-1996; 96CA-02190194.

XX PF 13-NOV-1996; 96CA-02190194.

XX PR 13-NOV-1996; 96CA-02190194.

XX (LIU/) LIU J H.

XX PA (SELI/) SELINGER L B.

XX PA (MOLO/) MOLONEY M M.

XX PA (FORS/) FORSBERG C W.

XX PA (CHEN/) CHENG K.

XX PA (HUYX/) HU Y.

XX LIU JH, Selinger LB, Moloney MM, Cheng K, Hu Y, Forsberg CW;

XX WPI; 1998-428424/37.













[illegible]

polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIP0 at <http://www.wipo.int/pub/published/pct/sequences>.

RESULT	38
ABG16236	
ID	ABG16236 standard; protein; 930 AA.
XX	
AC	ABG16236;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Novel human diagnostic protein #16227.
XX	
KW	Human; chromosome mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US008631.
XX	
PR	31-MAR-2000; 2000US-00540217.
PR	23-AUG-2000; 2000US-00649167.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Dzmanac RT, Liu C, Tang YT;
XX	

```
DR WPI; 2001-639362/73.
DR N-PSDB; AAS80423.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 46595; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridization probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 930 AA;
XX
Query Match 7.2%; Score 124; DB 4; Length 930;
Best Local Similarity 20.8%; Pred. No. 0.2; Indels 98; Gaps 19;
Matches 80; Conservative 65; Mismatches 141;
XX
QY 2 GSGSGGSSSTPNHPKVLVPTQNNLQAVPQANASQAQNAF-----QAQNAPOAQN 56
DB 225 GLSAYDNSRSPHSPIATPSSQSS-SCSDAPMLSTVHSAKNTPSQSHSIQSPERSG 283
QY 57 APQVENAPQ-----AQNAF-----QVENAPQAVTTP-VPOPOSQKIDGSPDKIGSVKLKE 107
DB 284 SGSVGNSSRYSPSONSPIHIPRRSPAKTIAPQNAPRDESGRKSSFYDGGDQETAKT 343
QY 108 AQTL-----ELSRFTLVKLTGTPPKFDKVGKIIIEKDFVLNLSDINAEQLSGDGLIR 162
DB 344 GKFLKRFYDESRVFLLDGNTNTR---DKEASKEKSEKG-----RAEGEWEDQ 388
QY 163 RSDDLFYGYHDTNGKLVDAADKPSQVYVYDSEKRVNDNTSDKLTAT-----YRK--- 214
DB 389 BALDYF-----SDKES-----GXQKFNDSEGDTEETEDYRQPKSVLA 427
QY 215 ---EGFVYGSNPHTK-----FAARISKLGIVE-----IKFENG---QAQGSIKD 253
DB 428 DQKSFATASHRNTEEBGLKYKSVLKGNRSESGFREERQYKLG-ETGYVVERPSTTKD 486
QY 254 ---EXDGNAEFTIKGDTKQLEITPTESNRIIIAI-----LDQNKSYTPGMEKAIM 303
DB 487 KHKEEDKNSERTVKKETQSPQVKSEKLGKLDIFDYSPLPHKNLDAKES--TFREESPLR 544
QY 304 TKFIDSKAGNSDKVLIGEASDN 327
DB 545 IKMTASDSHRPEVKMAPVPLDD 569
XX
RESULT 39
ABB59487
ID ABB59487 standard; protein; 861 AA.
XX
AC ABB59487;
XX
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DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 5253.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmacological.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-556860/75.
XX
XX N-PSDB; ABL03590.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 5253; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 861 AA;
XX
Query Match 7.1%; Score 123.5; DB 4; Length 861;
Best Local Similarity 27.7%; Pred. No. 0.2;
Matches 38; Conservative 15; Mismatches 61; Indels 23; Gaps 3;
XX
QY 2 GSGSGGSSSTPNHPKVLVPTQNNLQAVPQANASQAQNAPOAQNAPQVNAPOVNAPOV 61
DB 641 GVSAGQTHQIKPKPKP-----RPRVPEPKPKPKPKPKPKPKPKPKPKPKPKPK 690
QY 62 NAFQANAPQVNAPOAVTTPVPOQSQKIDGSPDKIGSV-----KLKNAQTLKLS 114
DB 691 KAPRVKAPRVKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPKPK 744
QY 115 RFTLVKLTGTPPKFDKV 131
DB 745 RPRVPEPKPKPKPKPKPK 761
XX
RESULT 40
ABU35643
ID ABU35643 standard; protein; 599 AA.
XX
AC ABU35643;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #21170.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
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QY      122 LGT---PPKFDKVS GKKI---IBEKDFVLNLSQINAEQLSGDFLIIRSDDL-----F 168
Db      416 LDTCFQPROVERTDSDITVSVSSHASLLKEKINALNHQRIWSDIALKSDNTIKKSNFSRF 475

QY      169 Y-----GYHDTNGKMLVDAAKFSQVFFVYDEKRYND-----NISDKLTA 209
Db      476 YPENEYVATKYSDFLYSDTN-QSL--TSDRFSLDFDYTPKSRVNNYTPLRSTNFQNNAIS 532

QY      210 TYR 212
Db      533 NYR 535

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Job time : 209.087 secs

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